

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 7, 2006, 09:32:55 ; Search time 30 Seconds
(without alignments)
1196.041 Million cell updates/sec

Title: US-10-820-714a-1-HIS15
Perfect score: 2251
Sequence: 1 NDVARGIVKADVAQHSYGLY.....EVQAINVPVGQTFSIAIWN 434

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2242	99.6	434	2 US-09-985-689A-1	Sequence 1, Appli
2	2242	99.6	640	2 US-09-509-814A-6	Sequence 6, Appli
3	2242	99.6	640	2 US-09-920-954-6	Sequence 6, Appli
4	2237	99.4	640	2 US-09-509-814A-8	Sequence 8, Appli
5	2237	99.4	640	2 US-09-920-954-8	Sequence 8, Appli
6	2186	97.1	434	2 US-09-985-689A-2	Sequence 2, Appli
7	2178	96.8	639	2 US-09-509-814A-4	Sequence 4, Appli
8	2178	96.8	639	2 US-09-920-954-4	Sequence 4, Appli
9	2150	95.5	639	2 US-09-509-814A-1	Sequence 1, Appli
10	2150	95.5	639	2 US-09-920-954-1	Sequence 1, Appli
11	2150	95.5	640	2 US-09-509-814A-2	Sequence 2, Appli
12	2150	95.5	640	2 US-09-920-954-2	Sequence 2, Appli
13	2138	95.0	434	2 US-09-985-689A-6	Sequence 6, Appli
14	2125.5	94.4	433	2 US-09-985-689A-7	Sequence 7, Appli
15	2125.5	94.4	641	1 US-08-873-479-42	Sequence 42, Appli
16	1998.5	88.8	433	2 US-09-985-689A-5	Sequence 5, Appli
17	1994.5	88.6	433	2 US-09-985-689A-3	Sequence 3, Appli
18	1987.5	88.3	433	2 US-09-985-689A-4	Sequence 4, Appli
19	1986.5	88.2	433	2 US-09-104-623A-4	Sequence 4, Appli
20	1986.5	88.2	433	2 US-09-019-532-4	Sequence 4, Appli
21	1986.5	88.2	433	2 US-09-338-746-4	Sequence 4, Appli
22	1986.5	88.2	635	1 US-08-873-479-43	Sequence 43, Appli
23	1581.5	70.3	345	2 US-09-512-251A-10	Sequence 10, Appli
24	1581.5	70.3	345	2 US-09-515-150A-10	Sequence 10, Appli
25	1581.5	70.3	345	2 US-09-196-281-13	Sequence 13, Appli
26	1581.5	70.3	345	2 US-10-336-324-10	Sequence 10, Appli
27	452.5	20.1	659	2 US-08-894-818B-1	Sequence 1, Appli

28	452.5	20.1	659	2	US-09-445-472-12	Sequence 12, Appli
29	452.5	20.1	659	2	US-10-090-624-12	Sequence 12, Appli
30	452.5	20.1	659	2	US-09-841-553-1	Sequence 1, Appli
31	414	18.4	412	2	US-09-445-472-1	Sequence 1, Appli
32	414	18.4	412	2	US-10-090-624-1	Sequence 1, Appli
33	414	18.4	412	2	US-08-894-818B-3	Sequence 3, Appli
34	414	18.4	522	2	US-09-445-472-4	Sequence 4, Appli
35	414	18.4	522	2	US-10-090-624-4	Sequence 4, Appli
36	414	18.4	522	2	US-09-841-553-3	Sequence 3, Appli
37	414	18.4	654	2	US-08-894-818B-35	Sequence 35, Appli
38	414	18.4	654	2	US-09-445-472-16	Sequence 16, Appli
39	414	18.4	654	2	US-10-090-624-16	Sequence 16, Appli
40	414	18.4	654	2	US-09-841-553-35	Sequence 35, Appli
41	401	17.8	659	2	US-08-894-818B-5	Sequence 5, Appli
42	401	17.8	659	2	US-09-841-553-5	Sequence 5, Appli
43	343.5	15.3	734	2	US-09-000-016-4	Sequence 4, Appli
44	343.5	15.3	734	2	US-09-514-340-4	Sequence 4, Appli
45	343.5	15.3	823	2	US-09-000-016-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-985-689A-1
; Sequence 1, Application US/09985689A
; Patent No. 6803222
; GENERAL INFORMATION:
; APPLICANT: HATADA, YUJI
; APPLICANT: OGAWA, AKINORI
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIKA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483US0
; CURRENT APPLICATION NUMBER: US/09/985,689A
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-985-689A-1

Query Match 99.6%; Score 2242; DB 2; Length 434;
Best Local Similarity 99.8%; Pred. No. 4, 1e-174;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	NDVARGIVKADVAQHSYGLYGGQIVAVADTGLDTRNDSSMHEAPRGKITAYALGRTN	60
DB	1	NDVARGIVKADVAQHSYGLYGGQIVAVADTGLDTRNDSSMHEAPRGKITAYALGRTN	60
QY	61	NANDTNGHGTTHVAGSVLGNSTKMGAPQANLVFQSIIMDSGGGLGSLPSNLQTLFSQAYS	120
DB	61	NANDTNGHGTTHVAGSVLGNSTKMGAPQANLVFQSIIMDSGGGLGSLPSNLQTLFSQAYS	120
QY	121	AGARHTNSWGAANGVAYTTDSRNVDYVYKNDMTILFAAGNEGNGGTISAPGTAKNAI	180
DB	121	AGARHTNSWGAANGVAYTTDSRNVDYVYKNDMTILFAAGNEGNGGTISAPGTAKNAI	180
QY	181	TVGATENLRPSGVSADNINHVQSSRGPTKDGRIKPDVMAPGTIFILSARSLAPDSF	240
DB	181	TVGATENLRPSGVSADNINHVQSSRGPTKDGRIKPDVMAPGTIFILSARSLAPDSF	240
QY	241	WANHDSKYAYMGSTSMATPIVAGNVAQLREHFVKGRTIPKPSLLKAAIAGAADIGLY	300

Db 241 WANHDSKYAYMGSTSMATPIVAGNVAQLREHFVKNGRITPKPSLLKAALIAGAADIGLY 300
QY 301 PNGNGGWRVTLDKSLNVAYNNESSLSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 301 PNGNGGWRVTLDKSLNVAYNNESSLSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNWDGRNNVNFVFINAPOSGTYYTIEVQAYN 420
Db 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNWDGRNNVNFVFINAPOSGTYYTIEVQAYN 420
QY 421 VPGPQTFSLAIVN 434
Db 421 VPGPQTFSLAIVN 434
RESULT 2
US-09-509-814A-6
; Sequence 6, Application US/09509814A
; Patent No. 6376227
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUW
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT APPLICATION NUMBER: US/09/509,814A
; CURRENT FILING DATE: 2000-04-06
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-509-814A-6

Query Match 99.6%; Score 2242; DB 2; Length 640;
Best Local Similarity 99.8%; Pred. No. 7.le-174;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAQHSYGLYGOGQIVAVADTGLDTRNDSSMHEAPRGKITALYALGRTN 60
Db 207 NDVARGIVKADVAQHSYGLYGOGQIVAVADTGLDTRNDSSMHEAPRGKITALYALGRTN 266
QY 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 267 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 327 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
QY 181 TVGATENLRPSGVSADNINHVAQFSRSGPTKDGRIKPDVMAPGTFILSARSLAPDSFS 240
Db 387 TVGATENLRPSGVSADNINHVAQFSRSGPTKDGRIKPDVMAPGTFILSARSLAPDSFS 446
QY 241 WANHDSKYAYMGSTSMATPIVAGNVAQLREHFVKNGRITPKPSLLKAALIAGAADIGLY 300
Db 447 WANHDSKYAYMGSTSMATPIVAGNVAQLREHFVKNGRITPKPSLLKAALIAGAADIGLY 506
QY 301 PNGNGGWRVTLDKSLNVAYNNESSLSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 507 PNGNGGWRVTLDKSLNVAYNNESSLSQKATYSFTATAGKPLKISLVWSDAPASTTA 566

QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNWDGRNNVNFVFINAPOSGTYYTIEVQAYN 420
Db 567 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNWDGRNNVNFVFINAPOSGTYYTIEVQAYN 626
QY 421 VPGPQTFSLAIVN 434
Db 627 VPGPQTFSLAIVN 640
RESULT 3
US-09-920-954-6
; Sequence 6, Application US/09920954
; Patent No. 6759228
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUW
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT APPLICATION NUMBER: US/09/920,954
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/509,814
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-920-954-6

Query Match 99.6%; Score 2242; DB 2; Length 640;
Best Local Similarity 99.8%; Pred. No. 7.le-174;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAQHSYGLYGOGQIVAVADTGLDTRNDSSMHEAPRGKITALYALGRTN 60
Db 207 NDVARGIVKADVAQHSYGLYGOGQIVAVADTGLDTRNDSSMHEAPRGKITALYALGRTN 266
QY 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 267 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 327 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
QY 181 TVGATENLRPSGVSADNINHVAQFSRSGPTKDGRIKPDVMAPGTFILSARSLAPDSFS 240
Db 387 TVGATENLRPSGVSADNINHVAQFSRSGPTKDGRIKPDVMAPGTFILSARSLAPDSFS 446
QY 241 WANHDSKYAYMGSTSMATPIVAGNVAQLREHFVKNGRITPKPSLLKAALIAGAADIGLY 300
Db 447 WANHDSKYAYMGSTSMATPIVAGNVAQLREHFVKNGRITPKPSLLKAALIAGAADIGLY 506
QY 301 PNGNGGWRVTLDKSLNVAYNNESSLSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 507 PNGNGGWRVTLDKSLNVAYNNESSLSQKATYSFTATAGKPLKISLVWSDAPASTTA 566
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNWDGRNNVNFVFINAPOSGTYYTIEVQAYN 420
Db 567 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNWDGRNNVNFVFINAPOSGTYYTIEVQAYN 626
QY 421 VPGPQTFSLAIVN 434

Db 627 VPVGPQTFSLAIVN 640
|||||

RESULT 4

US-09-509-814A-8
; Sequence 8, Application US/09509814A

; Patent No. 6376227

; GENERAL INFORMATION:

; APPLICANT: TAKAIWA, MIKIO

; APPLICANT: OKUDA, MITSUYOSHI

; APPLICANT: SAEKI, KATSUHIISA

; APPLICANT: KUBOTA, HIROMI

; APPLICANT: HITOMI, JUN

; APPLICANT: KAGEYAMA, YASUSHI

; APPLICANT: SHIKATA, SHITSUM

; APPLICANT: NOMURA, MASAFUMI

; TITLE OF INVENTION: ALKALINE PROTEASE

; FILE REFERENCE: 0327-0832-OPCT

; CURRENT APPLICATION NUMBER: US/09/509,814A

; PRIOR FILING DATE: 2000-04-06

; PRIOR APPLICATION NUMBER: PCT/JP98/04528

; PRIOR FILING DATE: 1998-10-07

; PRIOR APPLICATION NUMBER: JP 9-274570

; PRIOR FILING DATE: 1997-06-08

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 8

; LENGTH: 640

; TYPE: PRT

; ORGANISM: Bacillus sp.

US-09-509-814A-8

Query Match 99.4%; Score 2237; DB 2; Length 640;

Best Local Similarity 99.5%; Pred. No. 1.8e-173;

Matches 432; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60

Db 207 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 266

QY 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120

Db 267 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 326

QY 121 AGARIHTNSWGAANGVAYTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180

Db 327 AGARIHTNSWGAANGVAYTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386

QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSF 240

Db 387 TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSF 446

QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300

Db 447 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 506

QY 301 PNGNGGWRVTLDKSLNAVYVNESSLSSTSKATYSFTATAGKPLKISLVMSDAPASTTA 360

Db 507 PNGNGGWRVTLDKSLNAVYVNESSLSSTSKATYSFTATAGKPLKISLVMSDAPASTTA 566

QY 361 SVTLVNDLDLVTAPNGTQYVGNDFTSYNDNDGNNVNFVINAPOSQGTITIEVQAYN 420

Db 567 SVTLVNDLDLVTAPNGTQYVGNDFTSYNDNDGNNVNFVINAPOSQGTITIEVQAYN 626

QY 421 VPVGPQTFSLAIVN 434

Db 627 VPVGPQTFSLAIVN 640

RESULT 5

US-09-920-954-8

; Sequence 8, Application US/09920954

; Patent No. 6759228

; GENERAL INFORMATION:

; APPLICANT: TAKAIWA, MIKIO

; APPLICANT: OKUDA, MITSUYOSHI

; APPLICANT: SAEKI, KATSUHIISA

; APPLICANT: KUBOTA, HIROMI

; APPLICANT: HITOMI, JUN

; APPLICANT: KAGEYAMA, YASUSHI

; APPLICANT: SHIKATA, SHITSUM

; APPLICANT: NOMURA, MASAFUMI

; TITLE OF INVENTION: ALKALINE PROTEASE

; FILE REFERENCE: 0327-0832-OPCT

; CURRENT APPLICATION NUMBER: US/09/920,954

; PRIOR FILING DATE: 2001-08-03

; PRIOR APPLICATION NUMBER: 09/509,814

; PRIOR FILING DATE: 2000-04-06

; PRIOR APPLICATION NUMBER: PCT/JP98/04528

; PRIOR FILING DATE: 1998-10-07

; PRIOR APPLICATION NUMBER: JP 9-274570

; PRIOR FILING DATE: 1997-06-08

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 8

; LENGTH: 640

; TYPE: PRT

; ORGANISM: Bacillus sp.

US-09-920-954-8

Query Match 99.4%; Score 2237; DB 2; Length 640;

Best Local Similarity 99.5%; Pred. No. 1.8e-173;

Matches 432; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60

Db 207 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 266

QY 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120

Db 267 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 326

QY 121 AGARIHTNSWGAANGVAYTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180

Db 327 AGARIHTNSWGAANGVAYTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386

QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSF 240

Db 387 TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSF 446

QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300

Db 447 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 506

QY 301 PNGNGGWRVTLDKSLNAVYVNESSLSSTSKATYSFTATAGKPLKISLVMSDAPASTTA 360

Db 507 PNGNGGWRVTLDKSLNAVYVNESSLSSTSKATYSFTATAGKPLKISLVMSDAPASTTA 566

QY 361 SVTLVNDLDLVTAPNGTQYVGNDFTSYNDNDGNNVNFVINAPOSQGTITIEVQAYN 420

Db 567 SVTLVNDLDLVTAPNGTQYVGNDFTSYNDNDGNNVNFVINAPOSQGTITIEVQAYN 626

QY 421 VPVGPQTFSLAIVN 434

Db 627 VPVGPQTFSLAIVN 640

RESULT 6

US-09-985-689A-2

; Sequence 2, Application US/09985689A

; Patent No. 6803222

; GENERAL INFORMATION:

; APPLICANT: HATADA, YUJI

; APPLICANT: OGAWA, AKINORI

; APPLICANT: KAGEYAMA, YASUSHI

```
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NORIYUKI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHISA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483USO
; CURRENT APPLICATION NUMBER: US/09/985,689A
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-985-689A-2

Query Match          97.1%; Score 2186; DB 2; Length 434;
Best Local Similarity 96.3%; Pred. No. 1.5e-169;
Matches 418; Conservative 13; Mismatches 3; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGOGQIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQHSYGLYGOGQIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSSGGLGGLPSNLQTLFSQAYS 120
Db 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSSGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARIHTNSWGAANGAYTTDSRNVDVYRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSWGAANGAYTTDSRNVDVYRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSYADNINHVAQFSRGTGKGRIPKPDVMAPGTIFLSARSLAPDSFS 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSRGTGKGRIPKPDVMAPGTIFLSARSLAPDSFS 240
QY 241 WANHDSKYAYMGTSMTATPIVAGNVAQFSLTSQKATYSFTATAGKPLKISLVWSDAPASTTA 300
Db 241 WANHDSKYAYMGTSMTATPIVAGNVAQFSLTSQKATYSFTATAGKPLKISLVWSDAPASTTA 300
QY 301 PNGNCGWRVTLDKSLNVAIVNNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 301 PNGNCGWRVTLDKSLNVAIVNNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 360
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNWDGRNNVNFVFINAPQSGTYTIEVQAYN 420
Db 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNWDGRNNVNFVFINAPQSGTYTIEVQAYN 420
QY 421 VPVGPQTFSLAIVN 434
Db 421 VPVGPQNFSLAIVN 434

RESULT 7
US-09-509-814A-4
; Sequence 4, Application US/09509814A
; Patent No. 6376227
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUM
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-0PCT
; CURRENT FILING DATE: 2001-08-03
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
```

```
; CURRENT APPLICATION NUMBER: US/09/509,814A
; CURRENT FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-509-814A-4

Query Match          96.8%; Score 2178; DB 2; Length 639;
Best Local Similarity 96.1%; Pred. No. 1.1e-168;
Matches 417; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGOGQIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 206 NDVARGIVKADVAQSSYGLYGOGQIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 265
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSSGGLGGLPSNLQTLFSQAYS 120
Db 266 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSSGGLGGLPSNLQTLFSQAYS 325
QY 121 AGARIHTNSWGAANGAYTTDSRNVDVYRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
Db 326 AGARIHTNSWGAANGAYTTDSRNVDVYRKNDMTILFAAGNERPNGGTISAPGTAKNAI 385
QY 181 TVGATENLRPSFGSYADNINHVAQFSRGTGKGRIPKPDVMAPGTIFLSARSLAPDSFS 240
Db 386 TVGATENLRPSFGSYADNINHVAQFSRGTGKGRIPKPDVMAPGTIFLSARSLAPDSFS 445
QY 241 WANHDSKYAYMGTSMTATPIVAGNVAQFSLTSQKATYSFTATAGKPLKISLVWSDAPASTTA 300
Db 446 WANHDSKYAYMGTSMTATPIVAGNVAQFSLTSQKATYSFTATAGKPLKISLVWSDAPASTTA 505
QY 301 PNGNCGWRVTLDKSLNVAIVNNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 506 PNGNCGWRVTLDKSLNVAIVNNESSLSSTOKATYSFTATAGKPLKISLVWSDAPASTTA 565
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNWDGRNNVNFVFINAPQSGTYTIEVQAYN 420
Db 566 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNWDGRNNVNFVFINAPQSGTYTIEVQAYN 625
QY 421 VPVGPQTFSLAIVN 434
Db 626 VPVGPQNFSLAIVN 639

RESULT 8
US-09-920-954-4
; Sequence 4, Application US/09920954
; Patent No. 6759228
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUM
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-0PCT
; CURRENT APPLICATION NUMBER: US/09/920,954
; CURRENT FILING DATE: 2001-08-03
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
```



```
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-920-954-4

Query Match
Best Local Similarity 96.1%; Pred. No. 1.le-168;
Matches 417; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGGOIVAVADTGLDGTGRNDSHHEAPRGKITAYALGRTN 60
Db 206 NDVARGIVKADVAQHSYGLYGGOIVAVADTGLDGTGRNDSHHEAPRGKITAYALGRTN 265
QY 61 NANDTNGHGHVAGSVLGNSTNGKMGAPQANLVFQSDSSGGLGGLPSNLQTLFSQAYS 120
Db 266 NANDTNGHGHVAGSVLGNSTNGKMGAPQANLVFQSDSSGGLGGLPSNLQTLFSQAYS 325
QY 121 AGARIHTNSWGAANVAGYTTDSRNVDDYVRKNDMTILPAAGNEGPNNGGTISAPGTAKNAI 180
Db 326 AGARIHTNSWGAANVAGYTTDSRNVDDYVRKNDMTILPAAGNEGPNNGGTISAPGTAKNAI 385
QY 181 TVGATENLRPSFGSVADNINHVAQFSRSGTGDGRIPKDPVMAFGTFILSARSLAPDSSF 240
Db 386 TVGATENLRPSFGSVADNINHVAQFSRSGTGDGRIPKDPVMAFGTFILSARSLAPDSSF 445
QY 241 WANHDSKYAYMGTSMTATPIVAGNVQAQLREHFVNRGITPKPSLLKAALIAGAADIGLGY 300
Db 446 WANHDSKYAYMGTSMTATPIVAGNVQAQLREHFVNRGITPKPSLLKAALIAGADVGLGY 505
QY 301 PNGNCGWRVTLDKSLNVAYVNESSLSQATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 506 PNGNCGWRVTLDKSLNVAYVNESSLSQATYSFTATAGKPLKISLVWSDAPASTTA 565
QY 361 SVTLVNDLVLVTPAGTGYVNDFTSPYNDWNGNENNVFINAPQSGTITIEVOAYN 420
Db 566 SVTLVNDLVLVTPAGTGYVNDFTSPYNDWNGNENNVFINAPQSGTITIEVOAYN 625

QY 421 VPGVGPOTFSLAVN 434
Db 626 VPGVGPOTFSLAVN 639

RESULT 9
US-09-509-814A-1
; Sequence 1, Application US/09509814A
; Patent No. 6376227
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUM
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT APPLICATION NUMBER: US/09/509,814A
; CURRENT FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Bacillus sp.
```

```
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (23)..(23)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (29)..(29)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (32)..(32)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (46)..(46)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (47)..(47)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (53)..(53)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (70)..(70)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (74)..(74)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (89)..(89)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (102)..(102)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (105)..(105)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (128)..(128)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (130)..(130)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (131)..(131)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (132)..(132)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (133)..(133)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (146)..(146)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (148)..(148)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (160)..(160)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (165)..(165)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (172)..(172)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (183)..(183)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (187)..(187)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (188)..(188)
; OTHER INFORMATION: Xaa is any amino acid
```

```

; NAME/KEY: misc.feature
; LOCATION: (189)..(189)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: (194)..(194)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: (286)..(286)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: (306)..(306)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: (324)..(324)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: (431)..(431)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: (501)..(501)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: (531)..(531)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: (541)..(541)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: (584)..(584)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: (591)..(591)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: (592)..(592)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: (594)..(594)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: (595)..(595)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: (596)..(596)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: (611)..(611)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: (632)..(632)
; OTHER INFORMATION: Xaa is any amino acid
US-09-509-814A-1
Query Match 95.5%; Score 2150; DB 2; Length 639;
Best Local Similarity 96.1%; Pred. No. 2.1e-166;
Matches 417; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 206 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 265
QY 61 NANDTNGHGHVAGSVGLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 266 NANDTNGHGHVAGSVGLNGSTNKGMAPQANLVFQSIMDSXGGLGGLPSNLQTLFSQAYS 325
QY 121 AGARHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEPNGGTISAPGTAKNAI 180
Db 326 AGARHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEPNGGTISAPGTAKNAI 385
QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFFILSARSSLAPDSF 240
```

```

Db 386 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFFILSARSSLAPDSF 445
QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKRGIITPKPSLLKAALIAGAADIIGLY 300
Db 446 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKRGIITPKPSLLKAALIAGAADXGLGY 505
QY 301 PNGNQGWGRVTLDKSLNVAIYVNESSLSTSKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 506 PNGNQGWGRVTLDKSLNVAIYVNESSLSTSKATYKFTATAGKPLKISLVWSDAPASTTA 565
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNDGRRNVNFVINAPOSCTTYTIEVQYN 420
Db 566 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNDGRRNVNFVINAPOSCTTYTIEVQYN 625
QY 421 VPVGPQTFSLAIVN 434
Db 626 VPVGPQTFSLAIVN 639
RESULT 10
US-09-920-954-1
; Sequence 1, Application US/09920954
; Patent No. 6759228
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIKA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: SHIKATA, SHITSUMI
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCI
; CURRENT APPLICATION NUMBER: US/09/920,954
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/509,814
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Bacillus sp.
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (23)..(23)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: (29)..(29)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: (32)..(32)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: (46)..(46)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: (47)..(47)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: (53)..(53)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: (70)..(70)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: (74)..(74)
```

OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (89)..(89)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (102)..(102)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (105)..(105)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (128)..(128)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (130)..(130)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (131)..(131)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (132)..(132)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (133)..(133)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (146)..(146)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (148)..(148)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (160)..(160)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (165)..(165)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (172)..(172)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (183)..(183)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (187)..(187)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (188)..(188)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (189)..(189)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (194)..(194)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (286)..(286)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (306)..(306)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (324)..(324)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (369)..(369)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (431)..(431)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (501)..(501)
OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc feature
LOCATION: (531)..(531)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (541)..(541)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (584)..(584)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (591)..(591)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (592)..(592)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (594)..(594)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (595)..(595)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (611)..(611)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (632)..(632)
OTHER INFORMATION: Xaa is any amino acid
US-09-920-954-1

Query Match 95.5%; Score 2150; DB 2; Length 639;
Best Local Similarity 96.1%; Pred. No. 2,1e-166;
Matches 417; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB 206 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 265
QY 61 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQIMDSXGGLGPSNLQTLFSQAYS 120
DB 266 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQIMDSXGGLGPSNLQTLFSQAYS 325
QY 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 326 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 385
QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVWAPGTILSARSSLAPDSSF 240
DB 386 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVWAPGTILSARSSLAPDSSF 445
QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
DB 446 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 505
QY 301 PNGNQGWGRVTLDKSLNVAIVNNESSLSQSKATYSFTATAGKPLKISLWSDAPASTTA 360
DB 506 PNGNQGWGRVTLDKSLNVAIVNNESSLSQSKATYSFTATAGKPLKISLWSDAPASTTA 565
QY 361 SVTLVNDLILVITAPNGTOYVGNDFTPSYNDWNWGRNNVENVFINAPQSGTYTIEQAYN 420
DB 566 SVTLVNDLILVITAPNGTOYVGNDFTPSYNDWNWGRNNVENVFINAPQSGTYTIEQAYN 625
QY 421 VPVGPOTFSLAIWN 434
DB 626 VPVGPOTFSLAIWN 639

RESULT 11
US-09-509-814A-2
; Sequence 2, Application US/09509814A
; Patent No. 6376227

```
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUW
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT APPLICATION NUMBER: US/09/509,814A
; CURRENT FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (24)..(24)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (30)..(30)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (33)..(33)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (47)..(47)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (48)..(48)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (54)..(54)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (71)..(71)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (75)..(75)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (90)..(90)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (103)..(103)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (106)..(106)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (129)..(129)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (131)..(131)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (132)..(132)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (133)..(133)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (597)..(597)
; OTHER INFORMATION: Xaa is any amino acid
; LOCATION: (134)..(134)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (147)..(147)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (149)..(149)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (161)..(161)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (166)..(166)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (173)..(173)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (184)..(184)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (188)..(188)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (189)..(189)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (190)..(190)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (195)..(195)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (287)..(287)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (307)..(307)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (325)..(325)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (370)..(370)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (432)..(432)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (502)..(502)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (532)..(532)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (542)..(542)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (585)..(585)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (592)..(592)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (593)..(593)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (595)..(595)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (596)..(596)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (597)..(597)
```

```
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (612)..(612)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (633)..(633)
; OTHER INFORMATION: Xaa is any amino acid
US-09-509-814A-2

Query Match      95.5%; Score 2150; DB 2; Length 640;
Best Local Similarity 96.1%; Pred. No. 2.1e-166;
Matches 417; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAHQSYGLYGQGIIVAVADTGLDTCGRNDSSMHEAPRGKITALYALGRTN 60
DB 207 NDVARGIVKADVAHQSYGLYGQGIIVAVADTGLDTCGRNDSSMHEAPRGKITALYALGRTN 266

QY 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 267 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSXGGLGGLPSNLQTLFSQAYS 326

QY 121 AGARIHTNSGAAVNGAYTTDSNRVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 327 AGARIHTNSGAAVNGAYTTDSNRVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386

QY 181 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPGTTILSARSLAPDSF 240
DB 387 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPGTTILSARSLAPDSF 446

QY 241 WANHDSKYAMGTSWATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALIAGAADTGLGY 300
DB 447 WANHDSKYAMGTSWATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALIAGAADTGLGY 506

QY 301 PNGNQGWGRVTLDKSLNVAIVNESSLSSTSQKATYFTATAGKPLKISLVWSDAPASTTA 360
DB 507 PNGNQGWGRVTLDKSLNVAIVNESSLSSTSQKATYFTATAGKPLKISLVWSDAPASTTA 566

QY 361 SVTLVNDLVLVTAPNGTOYVGNDFTPSYNDKNDGRNVENFINAPQSGTYYTIEVQAYN 420
DB 567 SVTLVNDLVLVTAPNGTXYVGNDFXXPPXXNNDGRNVENFINXPSQSGTYYTIEVQAYN 626

QY 421 VPGVPOTFSLAIVN 434
DB 627 VPGVPQXFLAIVN 640

RESULT 12
US-09-920-954-2
; Sequence 2, Application US/09920954
; Patent No. 6759228
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUM
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT APPLICATION NUMBER: US/09/920,954
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/509,814
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 640
```

```
; TYPE: PRT
; ORGANISM: Bacillus sp.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (24)..(24)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (30)..(30)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (33)..(33)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (47)..(47)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (48)..(48)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (54)..(54)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (71)..(71)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (75)..(75)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (90)..(90)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (103)..(103)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (106)..(106)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (129)..(129)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (131)..(131)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (132)..(132)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (133)..(133)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (134)..(134)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (147)..(147)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (149)..(149)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (161)..(161)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (166)..(166)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (173)..(173)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (184)..(184)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
```

LOCATION: (188)..(188)
NAME/KEY: misc feature
LOCATION: (189)..(189)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (190)..(190)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (195)..(195)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (287)..(287)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (307)..(307)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (325)..(325)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (370)..(370)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (432)..(432)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (502)..(502)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (532)..(532)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (542)..(542)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (585)..(585)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (592)..(592)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (593)..(593)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (595)..(595)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (596)..(596)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (597)..(597)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (612)..(612)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: (633)..(633)
OTHER INFORMATION: Xaa is any amino acid

US-09-920-954-2
Query Match 95.5%; Score 2150; DB 2; Length 640;
Best Local Similarity 96.1%; Pred. No. 2.1e-166;
Matches 417; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVQAQSHYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITAIYALGRTN 60
DB 207 NDVARGIVKADVQAQSHYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITAIYALGRTN 266
QY 61 NANDTNGHGTAVGSLVNGSTNKGMAPOANLVFQSDVMDSGGLGGLPSNLQTLFSQAYS 120
DB 267 NANDTNGHGTAVGSLVNGSTNKGMAPOANLVFQSDVMDSGGLGGLPSNLQTLFSQAYS 326

QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
DB 327 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEXNGGTISAPGTAKNAI 386
QY 181 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF 240
DB 387 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF 446
QY 241 WANHDSKVAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALIAAGAADIGLY 300
DB 447 WANHDSKVAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALIAAGAADIGLY 506
QY 301 PNGNQWGRVTLDKSLNAVYNNSSLSSTQKATYSFTATAGKPLKISLVWSDAPASTTA 360
DB 507 PNGNQWGRVTLDKSLNAVYNNSSLSSTQKATYSFTATAGKPLKISLVWSDAPASTTA 566
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNDWGRNNVENVFINAPQSGTITIEVQAYN 420
DB 567 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNDWGRNNVENVFINAPQSGTITIEVQAYN 626
QY 421 VPVGPQTFSLAVN 434
DB 627 VPVGPQTFSLAVN 640

RESULT 13
US-09-985-689A-6
Sequence 6, Application US/09985689A
Patent No. 6803222
GENERAL INFORMATION:
APPLICANT: HATADA, YUJI
APPLICANT: OGAWA, AKINORI
APPLICANT: KAGEYAMA, YASUSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: ARAKI, HIROYUKI
APPLICANT: SUMITOMO, NOBUYUKI
APPLICANT: OKUDA, MITSUYOSHI
APPLICANT: SAKKI, KATSUHIISA
TITLE OF INVENTION: Alkaline proteases
FILE REFERENCE: 215483USO
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: JP P2000-355166
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: JP P2001-114048
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent in version 3.1
SEQ ID NO 6
LENGTH: 434
TYPE: PRT
ORGANISM: Bacillus sp.
US-09-985-689A-6

Query Match 95.0%; Score 2138; DB 2; Length 434;
Best Local Similarity 93.3%; Pred. No. 1.2e-165;
Matches 405; Conservative 19; Mismatches 10; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVQAQSHYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITAIYALGRTN 60
DB 1 NDVARGIVKADVQAQSHYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITAIYALGRTN 60
QY 61 NANDTNGHGTAVGSLVNGSTNKGMAPOANLVFQSDVMDSGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGTAVGSLVNGSTNKGMAPOANLVFQSDVMDSGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
DB 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMAVLFAGNEGNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF 240
DB 181 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF 240

QY 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
DB 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
QY 301 PNGNQGWGRVTLTKSLNVAVFNESSTLSQKATYSTAGTAKGPKLKISLWSDAPASTTA 360
DB 301 PNGNQGWGRVTLTKSLNVAVFNESSTLSQKATYSTAGTAKGPKLKISLWSDAPASTTA 360
QY 361 SVTLVNDLVLITAPNGTOYVGNDFSPYNDNWDGRNNVENVFINAPQSGTTYTIEVOAYN 420
DB 361 SVTLVNDLVLITAPNGTKYVGNDFTPAYDNNWDGRNNVENVFINAPQSGTTYTIEVOAYN 420
QY 421 VPVGPOTFSLAIVN 434
DB 421 VPQGPQAFSLAIVN 434

RESULT 14
US-09-985-689A-7
; Sequence 7, Application US/09985689A
; Patent No. 6803222
; GENERAL INFORMATION:
; APPLICANT: HATADA, YUJI
; APPLICANT: OGAWA, AKINORI
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SATO, TSUYOSHII
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483US0
; CURRENT APPLICATION NUMBER: US/09/985,689A
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-985-689A-7

Query Match 94.4%; Score 2125.5; DB 2; Length 433;
Best Local Similarity 93.5%; Pred. No. 1.2e-164;
Matches 406; Conservative 19; Mismatches 8; Indels 1; Gaps 1;
QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDGTGRNDSMHEAPRGKITALYALGRTN 60
DB 1 NDVARGIVKADVAQNFGLYGQGIIVAVADTGLDGTGRNDSMHEAPRGKITALYALGRTN 60
QY 61 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDPNGHGHVAGSVLGN-ATNKGMAPOANLVFQSIIMDSGGGLGGLPANLQTLFSQAYS 119
QY 121 AGARHTNSWGAANGVAYTTDSRNVDYVRKNDMTLLFAAGNEGPNGGTISAPGTAKNAI 180
DB 120 AGARHTNSWGAAPVNGAYTTDSRNVDYVRKNDMTLLFAAGNEGPNGGTISAPGTAKNAI 179
QY 181 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAPGTIFLSARSSLAPDSSF 240
DB 180 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAPGTIFLSARSSLAPDSSF 239
QY 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
DB 240 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADVGLGF 299
QY 301 PNGNQGWGRVTLTKSLNVAVFNESSTLSQKATYSTAGTAKGPKLKISLWSDAPASTTA 360

DB 300 PNGNQGWGRVTLTKSLNVAVFNESSTLSQKATYSTAGTAKGPKLKISLWSDAPGTTA 359
QY 361 SVTLVNDLVLITAPNGTOYVGNDFSPYNDNWDGRNNVENVFINAPQSGTTYTIEVOAYN 420
DB 360 SVTLVNDLVLITAPNGTKYVGNDFTPAYDNNWDGRNNVENVFINAPQSGTTYTIEVOAYN 419
QY 421 VPVGPOTFSLAIVN 434
DB 420 VPVSPQTFSLAIVH 433

RESULT 15
US-08-873-479-42
; Sequence 42, Application US/08873479
; Patent No. 5891701
; GENERAL INFORMATION:
; APPLICANT: Sloma, Alan
; APPLICANT: Lynne, Christianson
; TITLE OF INVENTION: Nucleic Acids Encoding A Polypeptide
; TITLE OF INVENTION: Having Protease Activity
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSES: No. 5891701o No. 5891701disk of No. 5891701th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,479
; FILING DATE: 12-JUN-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Agrie, Cheryl H
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 5251.000-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 641 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-873-479-42

Query Match 94.4%; Score 2125.5; DB 1; Length 641;
Best Local Similarity 93.5%; Pred. No. 2.1e-164;
Matches 406; Conservative 19; Mismatches 8; Indels 1; Gaps 1;
QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDGTGRNDSMHEAPRGKITALYALGRTN 60
DB 209 NDVARGIVKADVAQNFGLYGQGIIVAVADTGLDGTGRNDSMHEAPRGKITALYALGRTN 268
QY 61 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 269 NANDPNGHGHVAGSVLGN-ATNKGMAPOANLVFQSIIMDSGGGLGGLPANLQTLFSQAYS 327
QY 121 AGARHTNSWGAANGVAYTTDSRNVDYVRKNDMTLLFAAGNEGPNGGTISAPGTAKNAI 180
DB 328 AGARHTNSWGAAPVNGAYTTDSRNVDYVRKNDMTLLFAAGNEGPNGGTISAPGTAKNAI 387
QY 181 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAPGTIFLSARSSLAPDSSF 240

Db	388	TVGATENLRPSFGSYADNINHVAQFSSRGPTTRDGRIKPDVMAPGTYYILSARSSLAPDSSF	447
Qy	241	WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY	300
Db	448	WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGVTPKPSLLKAALIAGAADVGLGF	507
Qy	301	PNGNQGWGRVTLDKSLNVAYNNESSLSTSQKATYSFTATAGKPLKISLVMSDAPASTTA	360
Db	508	PNGNQGWGRVTLDKSLNVAFNETSPLSTSQKATYSFTAQAGKPLKISLVMSDAPGSTTA	567
Qy	361	SVTLVNDLVLITAPNGTQYVGNDFTSFYNDNWDGRNNVNFINAPQSGTYTIEVQAYN	420
Db	568	SVTLVNDLVLITAPNGTKYVGNDFTPYDNNWDGRNNVNFINAPQSGTYTIEVQAYN	627
Qy	421	VPVGPQTFSLAIVN	434
Db	628	VPVSPQTFSLAIVH	641

Search completed: April 7, 2006, 09:33:33
Job time : 31 secs

GenCore version 5.1.7

Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 7, 2006, 09:36:15 ; Search time 91 Seconds
(without alignments)

2095.499 Million cell updates/sec

Title: US-10-820-714a-1

Perfect score: 2247

Sequence: 1 NDVARGIVKADVAQSSYGLY.....EVQAYNPVGPQTFSLAIWN 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Geneseq 21.*

2: Geneseqp1980s.*

3: Geneseqp1990s.*

4: Geneseqp2000s.*

5: Geneseqp2001s.*

6: Geneseqp2002s.*

7: Geneseqp2003as.*

8: Geneseqp2003bs.*

9: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	2247	100.0	434 5	AAM50080 Bacillus
2	2247	100.0	434 7	ADY33778 Bacillus
3	2247	100.0	434 7	ADZ51757 Wild-type
4	2247	100.0	434 8	ADL25802 Bacillus
5	2247	100.0	434 8	ADM40771 Mature al
6	2247	100.0	434 8	ADL14427 Bacillus
7	2247	100.0	434 8	ADT49604 Bacillus
8	2247	100.0	640 2	AAV17090 Bacillus
9	2247	100.0	640 8	ADM40773 Alkaline
10	2247	100.0	640 8	ADL14437 Bacillus
11	2247	100.0	641 8	ADT49613 Bacillus
12	2242	99.8	434 8	ADM40780 Alkaline
13	2242	99.8	434 8	ADS14441 Bacillus
14	2242	99.8	640 2	AAV17091 Bacillus
15	2239	99.6	434 8	ADS14438 Bacillus
16	2239	99.6	434 8	ADL14442 Bacillus
17	2238	99.6	434 8	ADL14439 Bacillus
18	2232	99.3	434 8	ADS14440 Bacillus
19	2230	99.2	434 8	ADS14443 Bacillus
20	2225	99.0	434 8	ADS14444 Bacillus
21	2210	98.4	434 8	ADS14445 Alkaline
22	2195	97.7	436 8	ADM40787 Bacillus
23	2191	97.5	434 5	AAM50081 Bacillus
24	2191	97.5	434 7	ADZ51758 Mutant Ba

25	2191	97.5	434	8	ADM40779	Adm40779 Alkaline
26	2183	97.2	639	2	AAV17089	Aay17089 Bacillus
27	2155	95.9	639	2	AAV17087	Aay17087 An alkali
28	2155	95.9	640	2	AAV17088	Aay17088 An alkali
29	2143	95.4	434	5	AAM50085	Aam50085 Bacillus
30	2143	95.4	434	7	ADZ51762	Adz51762 Mutant Ba
31	2143	95.4	434	8	ADM40784	Adm40784 Alkaline
32	2130.5	94.8	433	8	ADS52078	Ads52078 Bacillus
33	2130.5	94.8	433	8	ADS52011	Ads52011 Bacillus
34	2129.5	94.8	433	8	ADS52082	Ads52082 Bacillus
35	2126.5	94.6	433	8	ADS52083	Ads52083 Bacillus
36	2125.5	94.6	433	5	AAM50086	Aam50086 Bacillus
37	2125.5	94.6	433	7	ADZ51763	Adz51763 Mutant Ba
38	2125.5	94.6	433	8	ADM40785	Adm40785 Alkaline
39	2125.5	94.6	433	8	ADS52010	Ads52010 Bacillus
40	2125.5	94.6	433	8	ADS52016	Ads52016 Bacillus
41	2125.5	94.6	433	8	ADS52001	Ads52001 Bacillus
42	2125.5	94.6	641	2	AAW89547	Aaw89547 Bacillus
43	2123.5	94.5	433	8	ADS52062	Ads52062 Bacillus
44	2123.5	94.5	433	8	ADS52054	Ads52054 Bacillus
45	2122.5	94.5	433	8	ADS52087	Ads52087 Bacillus

ALIGNMENTS

RESULT 1
AAM50080
ID AAM50080 standard; protein; 434 AA.
XX
AC AAM50080;
XX
DT 12-AUG-2002 (first entry)
XX
DE Bacillus sp KSM-KP43 alkaline protease protein fragment.
XX
KW Alkaline protease; detergent; laundry; bleaching; dishwasher.
XX
OS Bacillus sp.
XX
PN EP1209233-A2.
XX
PD 29-MAY-2002.
XX
PF 22-NOV-2001; 2001EP-00127851.
XX
PR 22-NOV-2000; 2000JP-00355166.
PR 12-APR-2001; 2001JP-00114048.
XX
PA (KAOS) KAO CORP.
XX
PI Hatada Y, Ogawa A, Kageyama Y, Sato T, Araki H, Sumitomo N;
PI Okuda M, Saeki K;
XX
DR WPI; 2002-437518/47.
XX
PT New modified alkaline proteases useful in detergent compositions.
XX
PS Claim 1; Page 10-11; 25pp; English.
XX
CC This invention describes novel Bacillus sp. alkaline proteases useful in
CC detergent compositions, especially in laundry, bleaching or automatic
CC dishwasher detergents. The novel proteases have an increased detergency
CC (34 - 38%) compared to prior art alkaline proteases (31 and 23%). This
CC sequence represents a fragment of the alkaline protease KP43 from
CC Bacillus sp strain KSM-KP43 which is used to create the modified protease
CC represented in AAM50090
XX
SQ Sequence 434 AA;

Query Match 100.0%; Score 2247; DB 5; Length 434;
Best Local Similarity 100.0%; Pred. No. 6.4e-159; Indels 0; Gaps 0;
Matches 434; Conservative 0; Mismatches 0;

PS		Claim 1; SEQ ID NO 1; 31pp; English.
XX		The invention relates to an alkaline protease having a fully defined
CC		sequence of 434 amino acids (I) given in the specification, or an amino
CC		acid sequence at least 80% homologous with (I), where an amino acid residue
CC		at position 65, 101, 163, 170, 171, 273, 320, 359 or 387 of (I) is
CC		selected from 16 amino acid residues. The amino acid residues at the
CC		corresponding positions are selected from: position 65: proline; position
CC		101: asparagine; position 163: histidine, aspartic acid, phenylalanine, or
CC		lysine, asparagine, serine, isoleucine, leucine, glutamine, threonine or
CC		valine; position 170: valine or leucine; position 171: alanine, glutamic
CC		acid, glycine or threonine; position 273: isoleucine, glycine or
CC		threonine; position 320: phenylalanine, valine, threonine, leucine,
CC		isoleucine or glycine; position 359: serine, leucine, valine, isoleucine
CC		or glutamic acid; and position 387: alanine, lysine, glutamine, glutamic
CC		acid, arginine or histidine. The alkaline protease is useful for the
CC		production of a detergent composition, such as laundry detergent, fiber
CC		modifiers, leather-treating agents, cosmetic compositions, bath
CC		additives, food modifiers and pharmaceutical compositions. The alkaline
CC		protease may also be used as bleaching detergent, hard surface cleaning
CC		detergent, pipe cleaner, artificial tooth cleaner, and as a sterilizing
CC		cleanser for medical tools. The new alkaline protease has a more potent
CC		proteolytic capacity, exhibiting excellent detergency for the removal of
CC		a complex stain, and has high secretion capacity. This sequence
CC		corresponds to the Bacillus sp. alkaline protease.
XX		
SQ		Sequence 434 AA;
Query Match		100.0%; Score 2247; DB 7; Length 434;
Best Local Similarity		100.0%; Pred. No. 6.4e-159;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTGRNDSMHAEFRGKITALYALGRTN 60
DB	1	NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTGRNDSMHAEFRGKITALYALGRTN 60
QY	61	NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
DB	61	NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
QY	121	AGARIHTNSWGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPGGTTISAPGTAKNAI 180
DB	121	AGARIHTNSWGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPGGTTISAPGTAKNAI 180
QY	181	TVGATENLRPSFGSYADNINHVAFSSRGPTKDGRIKPDVMAPTFILSARSSLAPDSSF 240
DB	181	TVGATENLRPSFGSYADNINHVAFSSRGPTKDGRIKPDVMAPTFILSARSSLAPDSSF 240
QY	241	WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
DB	241	WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
QY	301	PNGNQGWGRVTLDKSLNVAYVNESSLSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
DB	301	PNGNQGWGRVTLDKSLNVAYVNESSLSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
QY	361	SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWDGRNNVENVFINAPQSGTYTIEVQAYN 420
DB	361	SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWDGRNNVENVFINAPQSGTYTIEVQAYN 420
QY	421	VPVGPQTFSLAIVN 434
DB	421	VPVGPQTFSLAIVN 434
RESULT 3		
ADZ51757		ADZ51757 standard; protein; 434 AA.
XX	XX	ADZ51757;
XX	XX	ADZ51757;
XX	XX	16-JUN-2005 (first entry)
XX	XX	
QY		1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTGRNDSMHAEFRGKITALYALGRTN 60
DB		1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTGRNDSMHAEFRGKITALYALGRTN 60
QY		61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
DB		61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
QY		121 AGARIHTNSWGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPGGTTISAPGTAKNAI 180
DB		121 AGARIHTNSWGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPGGTTISAPGTAKNAI 180
QY		181 TVGATENLRPSFGSYADNINHVAFSSRGPTKDGRIKPDVMAPTFILSARSSLAPDSSF 240
DB		181 TVGATENLRPSFGSYADNINHVAFSSRGPTKDGRIKPDVMAPTFILSARSSLAPDSSF 240
QY		241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
DB		241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
QY		301 PNGNQGWGRVTLDKSLNVAYVNESSLSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
DB		301 PNGNQGWGRVTLDKSLNVAYVNESSLSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
QY		361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWDGRNNVENVFINAPQSGTYTIEVQAYN 420
DB		361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWDGRNNVENVFINAPQSGTYTIEVQAYN 420
QY		421 VPVGPQTFSLAIVN 434
DB		421 VPVGPQTFSLAIVN 434
RESULT 2		
ADZ33778		ADZ33778 standard; protein; 434 AA.
XX	XX	ADZ33778;
XX	XX	ADZ33778;
XX	XX	05-MAY-2005 (first entry)
XX	XX	Bacillus species alkaline protease.
XX	XX	mutagenesis; alkaline protease; detergent; laundry; cosmetic; food;
XX	XX	bleaching detergent.
XX	XX	Bacillus sp.
XX	XX	EP1347044-A2.
XX	XX	24-SEP-2003.
XX	XX	21-MAR-2003; 2003EP-00006472.
XX	XX	22-MAR-2002; 2002JP-00081428.
XX	XX	06-JUN-2002; 2002JP-00165987.
XX	XX	18-OCT-2002; 2002JP-00304230.
XX	XX	18-OCT-2002; 2002JP-00304231.
XX	XX	(KAOS) KAO CORP.
XX	XX	Okuda M, Sato T, Saito K, Sumitomo N, Izawa Y, Saeki K;
XX	XX	Kobayashi T, Nomura M;
XX	XX	WPI; 2003-846540/79.
XX	XX	N-PSDB; ADY33779.
XX	XX	New alkaline protease having specific amino acid residue at a specific
XX	XX	position of its amino acid sequence, useful for producing detergent
XX	XX	compositions, laundry detergent, fiber modifiers, leather-treating agents
XX	XX	or pipe cleaners.

Db	301	PNGQHGGRVTLDKSLNVAYVNESSLSLTSQKATYSFTATAGKPLKISLVMSDAPASTTA	360
Qy	361	SVTLVNDLVLITAPNGTQVYVNDFTSPYNDNDGRNNVENVFINAPQSGTYTIEVQAYN	420
Db	361	SVTLVNDLVLITAPNGTQVYVNDFTSPYNDNDGRNNVENVFINAPQSGTYTIEVQAYN	420
Qy	421	VPVGPQTFSLAIVN	434
Db	421	VPVGPQTFSLAIVN	434
RESULT 5			
ID	ADM40771	standard; protein; 434 AA.	
XX	AC	ADM40771;	
XX	DT	01-JUL-2004 (first entry)	
XX	DE	Mature alkaline protease from Bacillus sp. KSM-KP43.	
XX	KW	alkaline protease; laundry detergent; bleaching agent; detergent;	
XX	KW	denture-cleaning agent; enzyme.	
XX	OS	Bacillus sp.; KSM-KP43.	
XX	PN	US2004072321-A1.	
XX	PD	15-APR-2004.	
XX	PF	09-JUN-2003; 2003US-00456479.	
XX	PR	26-JUN-2002; 2002JP-00186387.	
XX	PR	18-OCT-2002; 2002JP-00304232.	
XX	PA	(KAOS) KAO CORP.	
XX	PI	Sato T, Okuda M, Takimura Y, Sumitomo N, Nomura M, Kobayashi T;	
XX	DR	WPI; 2004-328572/30.	
XX	DR	N-PSDB; ADM40772.	
XX	PT	New alkaline protease having a mutant prepro sequence where amino acid	
XX	PT	residues at positions 52, 75 and 142 are substituted with another amino	
XX	PT	acid residue, useful as enzyme component of laundry detergents, or	
XX	PT	bleaching agents.	
XX	PS	Claim 1; SEQ ID NO 2; 29pp; English.	
XX	CC	The invention relates to an alkaline protease having a prepro sequence.	
XX	CC	The prepro sequence is a mutant sequence of SEQ ID NO: 1, or an amino	
XX	CC	acid sequence having 80% homology or higher to SEQ ID NO: 1, where amino	
XX	CC	acid residues at: (a) position 52 is substituted by aspartic acid or	
XX	CC	arginine; (b) position 75 is substituted by alanine or arginine; and (c)	
XX	CC	position 142 is substituted by lysine. The alkaline protease is useful as	
XX	CC	an enzyme which can be incorporated into laundry detergents, bleaching	
XX	CC	agents, detergents for cleaning hard surfaces or drainpipes, denture-	
XX	CC	cleaning agents, and detergents for sterilising medical apparatus. The	
XX	CC	present sequence represents mature alkaline protease from Bacillus sp.	
XX	CC	KSM-KP43.	
XX	SQ	Sequence 434 AA;	
Query Match			
Best Local Similarity 100.0%; Score 2247; DB 8; Length 434;			
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	NDVARGIVKADVAQSSYGLYQGQIVAVADTGLDTGRNDSMHEAFRGKITALVALGRTN	60
Db	1	NDVARGIVKADVAQSSYGLYQGQIVAVADTGLDTGRNDSMHEAFRGKITALVALGRTN	60
Qy	61	NANDTNGHGHVAGSVLNGSTNGKMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS	120

Db	61	NANDTNGHGHVAGSVLNGSTNGKMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS	120
Qy	121	AGARIHTNSWGAAGVAYTTDSRVDDYVRKNDWTLTILFAAGNEGPNGGTISAPGTAKNAI	180
Db	121	AGARIHTNSWGAAGVAYTTDSRVDDYVRKNDWTLTILFAAGNEGPNGGTISAPGTAKNAI	180
Qy	181	TVGATENLRPSFGSYADNINNHVAFSSRGPTKDGRIKPDVMAFGTFLSARSSLAPDSSF	240
Db	181	TVGATENLRPSFGSYADNINNHVAFSSRGPTKDGRIKPDVMAFGTFLSARSSLAPDSSF	240
Qy	241	WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALAGAADIGLGY	300
Db	241	WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALAGAADIGLGY	300
Qy	301	PNGQHGGRVTLDKSLNVAYVNESSLSLTSQKATYSFTATAGKPLKISLVMSDAPASTTA	360
Db	301	PNGQHGGRVTLDKSLNVAYVNESSLSLTSQKATYSFTATAGKPLKISLVMSDAPASTTA	360
Qy	361	SVTLVNDLVLITAPNGTQVYVNDFTSPYNDNDGRNNVENVFINAPQSGTYTIEVQAYN	420
Db	361	SVTLVNDLVLITAPNGTQVYVNDFTSPYNDNDGRNNVENVFINAPQSGTYTIEVQAYN	420
Qy	421	VPVGPQTFSLAIVN	434
Db	421	VPVGPQTFSLAIVN	434
RESULT 6			
ID	ADS14427	standard; protein; 434 AA.	
XX	AC	ADS14427;	
XX	DT	30-DEC-2004 (first entry)	
XX	DE	Bacillus alkaline protease KP43 mature protein SEQ ID NO:1.	
XX	KW	protease; enzyme; alkaline protease; laundry detergent; KP43.	
XX	OS	Bacillus sp.; KSM-KP43.	
XX	PN	EP1466962-A1.	
XX	PD	13-OCT-2004.	
XX	PP	08-APR-2004; 2004EP-00008604.	
XX	PP	10-APR-2003; 2003JP-00106709.	
XX	PA	(KAOS) KAO CORP.	
XX	PI	Okuda M, Sato T, Takimura Y, Sumitomo N, Kobayashi T;	
XX	DR	WPI; 2004-711313/70.	
XX	DR	N-PSDB; ADS14428.	
XX	PT	New engineered alkaline protease, useful particularly in laundry	
XX	PT	detergents, comprising specified amino acids at particular positions.	
XX	PS	Claim 1; SEQ ID NO 1; 31pp; English.	
XX	CC	The invention relates to a novel alkaline protease. The new alkaline	
XX	CC	protease comprises an amino acid sequence in which one or more amino acid	
XX	CC	residues selected from those located at 7 specific positions within	
XX	CC	ASL1427, or at positions corresponding to these positions are: position	
XX	CC	15 (histidine), position 16 (threonine or glutamine), position 166	
XX	CC	(glycine), position 167 (valine), position 187 (serine), position 346	
XX	CC	(arginine), and position 405 (aspartic acid). The alkaline protease is	
XX	CC	useful in industry particularly in laundry detergents, but also e.g. in	
XX	CC	fibre modifying agents, leather processing agents, cosmetic compositions,	
XX	CC	bath additives, food-modifying agents, and pharmaceuticals. The present	
XX	CC	sequence represents the wild-type Bacillus sp. KSM-KP43 alkaline	

PR	07-OCT-1997;	97JP-00274570.	
XX	(KAOS) KAO CORP.		
PA	Takaiwa M, Okuda M, Saeki K, Kubota H, Hitomi J, Kageyama Y;		
XX	Shikata S, Nomura M;		
PI	WPI; 1999-287736/27.		
XX	N-PSDB; AAX37278.		
DR	Alkali protease from Bacillus used in washing powders.		
PT	Disclosure; Page 58-63; 71pp; Japanese.		
XX			
XX	The invention relates to alkaline proteases produced by strains of		
CC	Bacillus. The proteases ability to digest casein is not inhibited by		
CC	oleic acid and they have a high stability to oxidising agents. The		
CC	alkaline protease of the invention has the following properties: (a) it		
CC	is active over the pH range 4-13 and has at least 80% of its optimum		
CC	activity over the range pH 6-12; (b) after 30 minutes at 40 deg. C it is		
CC	stable over the pH range 6-11; c) its isoelectric point is 8.9-9.1; (d)		
CC	its ability to digest casein is not inhibited by oleic acid; (e) it has		
CC	molecular weight about 43,000 by SDS-PAGE. The alkaline proteases can be		
CC	used as enzymes in washing compositions for use in automatic dishwashers		
CC	and for washing clothes. The stability to oxidising agents allows the		
CC	enzyme to be an effective component of washing compositions including		
CC	bleaches. The present sequence represents an alkaline protease. (Updated		
CC	on 20-MAR-2003 to correct DR field.)		
XX			
XX	Sequence 640 AA;		
Query Match	100.0%;	Score 2247;	DB 2; Length 640;
Best Local Similarity	100.0%;	Pred. No. 1.1e-158;	
Matches	434;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	NDVARGIVADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN	60
DB	207	NDVARGIVADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN	266
QY	61	NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQIMDSGGGLGGLPSNLQTLFSQAYS	120
DB	267	NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQIMDSGGGLGGLPSNLQTLFSQAYS	326
QY	121	AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI	180
DB	327	AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI	386
QY	181	TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAPGTFLSARSSLAPDSSF	240
DB	387	TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAPGTFLSARSSLAPDSSF	446
QY	241	WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALIAGAADIGLGY	300
DB	447	WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALIAGAADIGLGY	506
QY	301	PNGNQGWGRVTLDKSLNVAYVNESSSLSTSQKATYFTATAGKPLKISLVMSDAPASTTA	360
DB	507	PNGNQGWGRVTLDKSLNVAYVNESSSLSTSQKATYFTATAGKPLKISLVMSDAPASTTA	566
QY	361	SVTLVNDLQVITAPNGTQVGNDFTPYNDNDGGRNVENVFINAPQSGTYTIEVQAYN	420
DB	567	SVTLVNDLQVITAPNGTQVGNDFTPYNDNDGGRNVENVFINAPQSGTYTIEVQAYN	626
QY	421	VPVGPOTFSLAIYN 434	
DB	627	VPVGPOTFSLAIYN 640	
RESULT 9			
ADMA40773			
ID	ADMA40773	standard; protein; 640 AA.	
XX			
AC	ADMA40773;		

XX	01-JUL-2004	(first entry)	
XX	Alkaline protease from Bacillus sp. KSM-KP43.		
DE	alkaline protease; laundry detergent; bleaching agent; detergent;		
KW	denture-cleaning agent; enzyme.		
XX	Bacillus sp.; KSM-KP43.		
OS	US2004072321-A1.		
XX	15-APR-2004.		
XX	09-JUN-2003; 2003US-00456479.		
XX	26-JUN-2002; 2002JP-00186387.		
PR	18-OCT-2002; 2002JP-00304232.		
XX	(KAOS) KAO CORP.		
PA	Sato T, Okuda M, Takimura Y, Sumitomo N, Nomura M, Kobayashi T;		
XX	WPI; 2004-328572/30.		
XX	N-PSDB; ADM40772.		
DR	New alkaline protease having a mutant prepro sequence where amino acid		
XX	residues at positions 52, 75 and 142 are substituted with another amino		
PT	acid residue, useful as enzyme component of laundry detergents, or		
PT	bleaching agents.		
XX	Disclosure; SEQ ID NO 4; 29pp; English.		
PS			
XX	The invention relates to an alkaline protease having a prepro sequence.		
CC	The prepro sequence is a mutant sequence of SEQ ID NO: 1, or an amino		
CC	acid residues having 80% homology or higher to SEQ ID NO: 1, where amino		
CC	acid residues at: (a) position 52 is substituted by aspartic acid or		
CC	arginine; (b) position 75 is substituted by alanine or arginine; and (c)		
CC	position 142 is substituted by lysine. The alkaline protease is useful as		
CC	an enzyme which can be incorporated into laundry detergents, bleaching		
CC	agents, detergents for cleaning hard surfaces or drainpipes, denture-		
CC	cleaning agents, and detergents for sterilising medical apparatus. The		
CC	present sequence represents alkaline protease from Bacillus sp. KSM-KP43.		
XX			
XX	Sequence 640 AA;		
Query Match	100.0%;	Score 2247;	DB 8; Length 640;
Best Local Similarity	100.0%;	Pred. No. 1.1e-158;	
Matches	434;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	NDVARGIVADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN	60
DB	207	NDVARGIVADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN	266
QY	61	NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQIMDSGGGLGGLPSNLQTLFSQAYS	120
DB	267	NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQIMDSGGGLGGLPSNLQTLFSQAYS	326
QY	121	AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI	180
DB	327	AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI	386
QY	181	TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAPGTFLSARSSLAPDSSF	240
DB	387	TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAPGTFLSARSSLAPDSSF	446
QY	241	WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALIAGAADIGLGY	300
DB	447	WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALIAGAADIGLGY	506
QY	301	PNGNQGWGRVTLDKSLNVAYVNESSSLSTSQKATYFTATAGKPLKISLVMSDAPASTTA	360
DB	507	PNGNQGWGRVTLDKSLNVAYVNESSSLSTSQKATYFTATAGKPLKISLVMSDAPASTTA	566
QY	361	SVTLVNDLQVITAPNGTQVGNDFTPYNDNDGGRNVENVFINAPQSGTYTIEVQAYN	420
DB	567	SVTLVNDLQVITAPNGTQVGNDFTPYNDNDGGRNVENVFINAPQSGTYTIEVQAYN	626
QY	421	VPVGPOTFSLAIYN 434	
DB	627	VPVGPOTFSLAIYN 640	
RESULT 9			
ADMA40773			
ID	ADMA40773	standard; protein; 640 AA.	
XX			
AC	ADMA40773;		


```
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTSFYNDNDGRNNVNFVFNAPQSGTYTIEVOAYN 420
Db 567 SVTLVNDLVLITAPNGTQYVGNDFTSFYNDNDGRNNVNFVFNAPQSGTYTIEVOAYN 626
QY 421 VPVGPQTFSLAIVN 434
Db 627 VPVGPQTFSLAIVN 640

RESULT 10
ADSL14437
ID ADSL14437 standard; protein; 640 AA.
XX
AC ADSL14437;
DT 30-DEC-2004 (first entry)
XX
DE Bacillus alkaline protease KP43.
XX
KW protease; enzyme; alkaline protease; laundry detergent; KP43.
XX
OS Bacillus sp.; KSM-KP43.
XX
FH Key Location/Qualifiers
FT Peptide 1..206
FT Protein 207..640
XX
PN EP1466962-A1.
XX
PD 13-OCT-2004.
XX
PF 08-APR-2004; 2004EP-00008604.
XX
PR 10-APR-2003; 2003JP-00106709.
XX
PA (KAOS ) KAO CORP.
XX
PI Okuda M, Sato T, Takimura Y, Sumitomo N, Kobayashi T;
DR WPI; 2004-711313/70.
DR N-PSDB; ADSL14428.
XX
PT New engineered alkaline protease, useful particularly in laundry
FT detergents, comprising specified amino acids at particular positions.
XX
PS Disclosure; SEQ ID NO 1; 31pp; English.
XX
CC The invention relates to a novel alkaline protease. The new alkaline
CC protease comprises an amino acid sequence in which one or more amino acid
CC residues selected from those located at 7 specific positions within
CC ADSL14427, or at positions corresponding to these positions are: position
CC 15 (histidine), position 16 (threonine or glutamine), position 166
CC (glycine), position 167 (valine), position 187 (serine), position 346
CC (arginine), and position 405 (aspartic acid). The alkaline protease is
CC useful in industry particularly in laundry detergents, but also e.g. in
CC fibre modifying agents, leather processing agents, cosmetic compositions,
CC bath additives, food-modifying agents, and pharmaceuticals. The present
CC sequence represents the wild-type Bacillus sp. KSM-KP43 alkaline
CC protease, KP43. The sequence is shown in the sequence listing as part of
CC SEQ ID NO:1
XX
SQ Sequence 640 AA;

Query Match 100.0%; Score 2247; DB 8; Length 640;
Best Local Similarity 100.0%; Pred. No. 1.1e-158;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 60
Db 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 266
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
```

```
Db 267 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARIHTNSGAAVNGAYTTTDSRNVDYVRKNDMTILFAAGNEGPNNGTISAPCTAKNAI 180
Db 327 AGARIHTNSGAAVNGAYTTTDSRNVDYVRKNDMTILFAAGNEGPNNGTISAPCTAKNAI 386
QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAFGTFTLSARSSLAPDSSF 240
Db 387 TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAFGTFTLSARSSLAPDSSF 446
QY 241 WANHDSKYAYMGTSNATPIVAGNVAQLREHFVKNRGITPKPSILKAALTAGADIIGLY 300
Db 447 WANHDSKYAYMGTSNATPIVAGNVAQLREHFVKNRGITPKPSILKAALTAGADIIGLY 506
QY 301 PNGNQGWRVTLDKSLNVAIVNNESSLSSTSQKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 507 PNGNQGWRVTLDKSLNVAIVNNESSLSSTSQKATYSFTATAGKPLKISLVMSDAPASTTA 566
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTSFYNDNDGRNNVNFVFNAPQSGTYTIEVOAYN 420
Db 567 SVTLVNDLVLITAPNGTQYVGNDFTSFYNDNDGRNNVNFVFNAPQSGTYTIEVOAYN 626
QY 421 VPVGPQTFSLAIVN 434
Db 627 VPVGPQTFSLAIVN 640

RESULT 11
ADT49613
ID ADT49613 standard; protein; 641 AA.
XX
AC ADT49613;
DT 30-DEC-2004 (first entry)
XX
DE Bacillus alkaline protease.
XX
KW Alkaline protease; detergent; fiber modification; leather processing;
KW cosmetic; bath additives; food-modification; pharmaceutical; enzyme.
XX
OS Bacillus sp. KSM-KP43.
XX
FH Key Location/Qualifiers
FT Peptide 1..206
FT Protein 207..641
FT /note= "specifically claimed mature protein (SEQ ID 1)"
XX
PN EP1466970-A1.
XX
PD 13-OCT-2004.
XX
PF 08-APR-2004; 2004EP-00008605.
XX
PR 10-APR-2003; 2003JP-00106708.
XX
PA (KAOS ) KAO CORP.
XX
PI Sato T, Okuda M, Koyama S, Izawa Y, Kobayashi T;
DR WPI; 2004-711317/70.
DR N-PSDB; ADT49605.
XX
PT New engineered alkaline protease with improved activity and thermal
PT stability, useful particularly in detergents such as laundry detergents.
XX
PS Disclosure; Page 19-25; 35pp; English.
XX
CC The invention relates to an alkaline protease and its encoding gene. The
CC alkaline protease can be expressed by standard recombinant methodology.
CC The alkaline protease is useful in the industry particularly in
CC detergents such as laundry detergents, but also in fiber modifying
```


OS Synthetic.
XX Key Location/Qualifiers
FH Misc-difference 187
FT /note= "Wild-type Asn substituted by Ser"
FT
PN EP1466962-A1.
XX
XX 13-OCT-2004.
XX
XX 08-APR-2004; 2004EP-00008604.
XX
XX 10-APR-2003; 2003JP-00106709.
XX
XX (KAOS) KAO CORP.
XX
XX Okuda M, Sato T, Takimura Y, Sumitomo N, Kobayashi T;
XX WPI; 2004-711313/70.
XX
XX New engineered alkaline protease, useful particularly in laundry
PT detergents, comprising specified amino acids at particular positions.
XX
XX Example 1; Page; 31pp; English.
XX
XX The invention relates to a novel alkaline protease. The new alkaline
CC protease comprises an amino acid sequence in which one or more amino acid
CC residues selected from those located at 7 specific positions within
CC ADS14427, or at positions corresponding to these positions are: position
CC 15 (histidine), position 16 (threonine or glutamine), position 166
CC (glycine), position 167 (valine), position 187 (serine), position 346
CC (arginine), and position 405 (aspartic acid). The alkaline protease is
CC useful in industry particularly in laundry detergents, but also e.g. in
CC fibre modifying agents, leather processing agents, cosmetic compositions,
CC bath additives, food-modifying agents, and pharmaceuticals. The present
CC sequence represents an alkaline protease variant of the invention. Note:
CC The present sequence is not represented in the specification, but has
CC been created by the indexer using sequence shown in ADS14427 and
CC information given in Example 1.
XX
XX Sequence 434 AA;
XX
XX Query Match 99.8%; Score 2242; DB 8; Length 434;
XX Best Local Similarity 99.8%; Pred. No. 1.5e-158;
XX Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAQSSYGLYGQGI VAVADTGLDTRNDSSMHEAFRGKITALYALGRN 60
DB 1 NDVARGIVKADVAQSSYGLYGQGI VAVADTGLDTRNDSSMHEAFRGKITALYALGRN 60
QY 61 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSGIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSGIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARLHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 121 AGARLHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPFGSYADNHNHVAQFSRGPTKDGRIKPDVMAFGTIFLSARSLAPDSSF 240
DB 181 TVGATESLRPFGSYADNHNHVAQFSRGPTKDGRIKPDVMAFGTIFLSARSLAPDSSF 240
QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIIGLY 300
DB 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIIGLY 300
QY 301 PNGNGQWGRVTLDKSLNVAIVNESSLSQATYSFTATAGKPLKISLVWSDAPASTTA 360
DB 301 PNGNGQWGRVTLDKSLNVAIVNESSLSQATYSFTATAGKPLKISLVWSDAPASTTA 360
QY 361 SVTLVNDLVLVITAPNGTQVGNDFTPSYNDNWDGRNNVENVPINAPQSGTYYIEVQAYN 420
DB 361 SVTLVNDLVLVITAPNGTQVGNDFTPSYNDNWDGRNNVENVPINAPQSGTYYIEVQAYN 420

QY 421 VPVGQPTESLAIVN 434
DB 421 VPVGQPTESLAIVN 434
RESULT 14
AAV17091
ID AAY17091 standard; protein; 640 AA.
XX
XX AAY17091;
XX
XX 20-MAR-2003 (revised)
DT 21-JUL-1999 (first entry)
XX
XX Bacillus alkaline protease.
XX
XX Alkaline protease; Bacillus; casein digestion; oleic acid; enzyme;
KW washing composition; oxidising agent.
XX
XX Bacillus sp.
XX
XX WO9918218-A1.
PN
XX
XX 15-APR-1999.
XX
XX 07-OCT-1998; 98WO-JP004528.
XX
XX 07-OCT-1997; 97JP-00274570.
XX
XX (KAOS) KAO CORP.
XX
XX Takaiwa M, Okuda M, Saeki K, Kubota H, Hitomi J, Kageyama Y;
PI Shikata S, Nomura M;
XX
XX WPI; 1999-287736/27.
DR
XX N-PSDB; AAX37279.
XX
XX Alkali protease from Bacillus used in washing powders.
XX
XX Disclosure; Page 63-68; 71pp; Japanese.
XX
XX The invention relates to alkaline proteases produced by strains of
CC Bacillus. The proteases ability to digest casein is not inhibited by
CC oleic acid and they have a high stability to oxidising agents. The
CC alkaline protease of the invention has the following properties: (a) it
CC is active over the pH range 4-13 and has at least 80% of its optimum
CC activity over the pH range 6-12; (b) after 30 minutes at 40 deg. C it is
CC stable over the pH range 6-11; c) its isoelectric point is 8.9-9.1; (d)
CC its ability to digest casein is not inhibited by oleic acid; (e) it has
CC molecular weight about 43,000 by SDS-PAGE. The alkaline proteases can be
CC used as enzymes in washing compositions for use in automatic dishwashers
CC and for washing clothes. The stability to oxidising agents allows the
CC enzyme to be an effective component of washing compositions including
CC bleaches. The present sequence represents an alkaline protease. (Updated
CC on 20-MAR-2003 to correct DR field.)
XX
XX Sequence 640 AA;
XX
XX Query Match 99.8%; Score 2242; DB 2; Length 640;
XX Best Local Similarity 99.8%; Pred. No. 2.5e-158;
XX Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAQSSYGLYGQGI VAVADTGLDTRNDSSMHEAFRGKITALYALGRN 60
DB 207 NDVARGIVKADVAQSSYGLYGQGI VAVADTGLDTRNDSSMHEAFRGKITALYALGRN 266
QY 61 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSGIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 267 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSGIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARLHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 121 AGARLHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180

Db 327 AGARIHTNSWGAAYNGAYTTDSERNVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTIFILSARSSLAPDSF 240
Db 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTIFILSARSSLAPDSF 446
Qy 241 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKRGITPKPSLKAALJAGAADIGLY 300
Db 447 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKRGITPKPSLKAALJAGAADIGLY 506
Qy 301 PNGNOGWGRVTLDKSLNVAYNSSSLSTSOKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 507 PNGNOGWGRVTLDKSLNVAYNSSSLSTSOKATYSFTATAGKPLKISLVWSDAPASTTA 566
Qy 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWNGRNNVNFINAPQSGTYYIEVOAYN 420
Db 567 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWNGRNNVNFINAPQSGTYYIEVOAYN 626
Qy 421 VPVGPQTFSIAIWN 434
Db 627 VPVGPQNFSLAIWN 640

RESULT 15
ADS14438
ID ADS14438 standard; protein; 434 AA.
XX AC
XX AC ADS14438;
DT 30-DEC-2004 (first entry)
XX DE Bacillus alkaline protease KP43 S15H/S16T mutant.
DE protease; enzyme; alkaline protease; laundry detergent; KP43; mutant;
KW mutein.
XX OS Bacillus sp.; KSM-KP43.
OS Synthetic.
XX FH Key Location/Qualifiers
FT Misc-difference 15 /note= "Wild-type Ser substituted by His"
FT Misc-difference 16 /note= "Wild-type Ser substituted by Thr"
FT
PN EP1466962-A1.
XX PD 13-OCT-2004.
XX PF 08-APR-2004; 2004EP-00008604.
XX PR 10-APR-2003; 2003JP-00106709.
XX PA (KAOS) KAO CORP.
XX PI Okuda M, Sato T, Takimura Y, Sumitomo N, Kobayaashi T;
XX WPI; 2004-711313/70.
XX
XX New engineered alkaline protease, useful particularly in laundry
XX detergents, comprising specified amino acids at particular positions.
XX
XX Example 1; Page; 31pp; English.

XX The invention relates to a novel alkaline protease. The new alkaline
XX protease comprises an amino acid sequence in which one or more amino acid
XX residues selected from those located at 7 specific positions within
XX ADS14427, or at positions corresponding to these positions are: position
XX 15 (histidine), position 16 (threonine or glutamine), position 166
XX (glycine), position 167 (valine), position 187 (serine), position 346
XX (arginine), and position 405 (aspartic acid). The alkaline protease is
XX useful in industry particularly in laundry detergents, but also e.g. in
XX fibre modifying agents, leather processing agents, cosmetic compositions,

CC bath additives, food-modifying agents, and pharmaceuticals. The present
CC sequence represents an alkaline protease variant of the invention. Note:
CC The present sequence is not represented in the specification, but has
CC been created by the indexer using sequence shown in ADS14427 and
CC information given in Example 1.
XX
SQ Sequence 434 AA;

Query Match 99.6%; Score 2239; DB 8; Length 434;
Best Local Similarity 99.5%; Pred. No. 2.5e-158;
Matches 432; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRN 60
Db 1 NDVARGIVKADVAQHTYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRN 60
Qy 61 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSIWDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSIWDSGGGLGGLPSNLQTLFSQAYS 120
Qy 121 AGARIHTNSWGAAYNGAYTTDSERNVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSWGAAYNGAYTTDSERNVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTIFILSARSSLAPDSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTIFILSARSSLAPDSF 240
Qy 241 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKRGITPKPSLKAALJAGAADIGLY 300
Db 241 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKRGITPKPSLKAALJAGAADIGLY 300
Qy 301 PNGNOGWGRVTLDKSLNVAYNSSSLSTSOKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 301 PNGNOGWGRVTLDKSLNVAYNSSSLSTSOKATYSFTATAGKPLKISLVWSDAPASTTA 360
Qy 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWNGRNNVNFINAPQSGTYYIEVOAYN 420
Db 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWNGRNNVNFINAPQSGTYYIEVOAYN 420
Qy 421 VPVGPQTFSIAIWN 434
Db 421 VPVGPQTFSIAIWN 434

Search completed: April 7, 2006, 09:37:55
Job time : 92 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 7, 2006, 09:39:04 ; Search time 40 Seconds
(without alignment)
1043.952 Million cell updates/sec

Title: US-10-820-714A-1

Perfect score: 2247

Sequence: 1 NDVARGIVKADVAQSSYGLY.....EVQAVNPVPGPTFSLAIVN 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	523.5	23.3	1743	2	Ti8279
2	497	22.1	1905	2	Ti8267
3	347.5	15.5	444	2	B83891
4	320.5	14.3	442	2	A69587
5	310.5	13.8	806	2	A41341
6	302.5	13.5	1398	2	T28159
7	283	12.6	580	2	S11890
8	281	12.5	419	1	S25835
9	280	12.5	799	2	G83753
10	279.5	12.4	1345	2	T29090
11	277	12.3	420	1	S23407
12	267	11.9	715	2	JC4908
13	263	11.7	1331	2	A72647
14	259.5	11.5	757	2	C84120
15	257.5	11.5	513	1	A35742
16	253.5	11.3	894	2	F69730
17	251	11.2	627	2	D75393
18	246.5	11.0	402	1	JU0332
19	246.5	11.0	534	1	JS0173
20	243	10.8	519	2	S71451
21	242.5	10.8	401	2	I39974
22	240	10.7	380	2	A49778
23	240	10.7	488	2	A1930
24	235.5	10.5	382	1	SUBSN
25	235	10.5	378	2	A33973
26	235	10.5	382	2	I39780
27	234	10.4	910	2	C69456
28	234	10.4	1374	2	D72593
29	232.5	10.3	525	2	G84406

alkaline proteinase
subtilisin (EC 3.4
serine proteinase
streptococcal Csa
subtilisin like pr
subtilisin (EC 3.4
hypothetical prote
intraluminal subti
subtilisin (EC 3.4
subtilisin (EC 3.4
subtilisin (EC 3.4
alkaline proteinase
subtilisin (EC 3.4
halolysin (EC 3.4
serine proteinase

30 231 10.3 321 1 S27501
31 230.5 10.3 379 1 SUBSCL
32 229.5 10.2 601 2 JC4576
33 227 10.1 1167 1 A35066
34 226.5 10.1 1118 2 H97298
35 225.5 10.0 381 2 JH0778
36 225.5 10.0 613 2 S75976
37 225.5 10.0 1052 2 T17093
38 223.5 9.9 381 1 SUBSI
39 223.5 9.9 381 1 SUBSS
40 223.5 9.9 381 2 JQ1487
41 222.5 9.9 275 2 JC1085
42 222 9.9 384 2 JC4802
43 221.5 9.9 272 2 A23624
44 221.5 9.9 530 2 A42605
45 221 9.8 1036 2 JC5568

RESULT 1
Ti8279
multidrug resistance transport protein - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: Ti8279
R:Shaulsky, G.; Loomis, W.F.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z18855
A:Accession: Ti8279
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1743 <SHA>
A:Cross-references: UNIPROT:Q23868; UNIPARC:UPI000013687D; EMBL:U60086; NID:g1399914; PIR
C:Genetics:
A:Gene: tagC

Query Match 23.3%; Score 523.5; DB 2; Length 1743;
Beat Local Similarity 27.9%; Pred. No. 3.5e-25;
Matches 165; Conservative 81; Mismatches 150; Indels 195; Gaps 24;

Qy 19 LVGQGIIVAVADTGLDTGR---NDS-----SMHEAFRGKITALYALGRTNANDTNGH 68
Db 314 LRKGQILUSIADTGLDGHCFSDSKYPIPLNSVNLNR-KVVTYITTSDDSKVDGH 372
Qy 69 GTHVAGSVLG-----NGSTNKGMAPQANLVFQIMDSGGGLGL--PSNLTQLFSQAY 119
Db 373 GTHICGSAAGTPEDSSVNISSFSGLATDAKIAF---FDLASGSSSLTPSDLKQLYQPLY 429
Qy 120 SAGARIHTNSGA-----AVNGAYTTDSRNVDDYVRKN-DMTILFAAGNEGPNGGTIS--A 172
Db 430 DAGARVHCDNSGVSVEGTGYSSTASIDDFLTPHDFILRAAGN---NEQVLSLIT 486
Qy 173 PGTAKNAITVGTATENLR-----PSFGSYADNI----- 199
Db 487 QSTAKNVITVGAHQTIHENYLTGDNINYOSSVDINQELICDFDSRYCNYTTAQCLES 546
Qy 200 -----NHVAQFSRSGPTKDKRIKPDVMAQPTFL 228
Db 547 NATTGLASCCPTILRKSVIDAANTOPLYNNENICFSKSGPTHGRKPKPALVAFGEYIT 606
Qy 229 SARSSLA-----PDSSFWANHSKYAYMGGTSMATPIVAGNVAQLREH-----F 272
Db 607 SARNSGANTTQCGDGL-PTNALLA-IGSTSMATSFAAAATTLIRQVLDVGYVPTGSI 664
Qy 273 VNRGITPKPILLKALITAGA-----ADTGLGPNGN-----QWGRVT 311
Db 665 VESNKLQPTGSLKALMINNAQLLNGTFLQITSSSITYPSNQVFENFAGSLVQWGAIR 724
Qy 312 LDKSINVAIVNNESS-----ADTGLGPNGN-----SLTSOKATVSEF-- 338
Db 725 MSNWLHVNNNNNNNNNTSGITKFDGIGGLDLRLVKNQWKEESTSGTNTSCFTYK 784

ALIGNMENTS

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowaka, A.; Seror, A.; Tanakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, A.; Tosato, V.; Uchiyama, K.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: D69730
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-806 <KUN>
A:Cross-references: UNIPARC:UPI0000060C20; GB:Z99123; GB:AL009126; NID:g2636240; PIDN:CAI
A:Experimental source: strain 168
C:Comment: The amino terminal sequence of the mature protein and a molecular weight of or
C:Genetics:
A:Gene: vpr
A:Start codon: TTG
C:Superfamily: microbial serine proteinase vpr; subtilisin homology
C:Keywords: hydrolase; serine proteinase
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-160/Domain: propeptide #status predicted <PRO>
F:180-548/Domain: subtilisin homology #status atypical <SBT>

Query Match 14.3%; Score 320.5; DB 2; Length 442;
Best Local Similarity 29.7%; Pred. No. 4.4e-13;
Matches 107; Conservative 50; Mismatches 104; Indels 99; Gaps 16;

QY 11 DVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRNTNAN-----D 64
DB 136 EVVRNGQITLGGTVAVVDTGL-----YHPDLEGR-----IGFADWVNQKTEPYD 183
QY 65 TNGHGTAVAGSVLNGSTN-----KGMAPQANLVFOSIMDSGGGLGSLPNSLQTLFSQAVS 120
DB 184 DNGHGTACADVASSGASSGQYRPAEPANLIGVKLVNKQS-GTLDIIIEGV----- 236
QY 121 AGARHTNSWGAENV-----GAYTDSRNVDVVRKND-----MTIL 157
DB 237 -----EWCIOYNEDNPEDIDMSLSLGDALRYDHEQEDPLVRAVEAWSAGIVVC 288
QY 158 FAAGNEGNGGTISAPGTAKNAITVGCATENLRPSFGSYADNINHVAFSSRGPTKDGRIK 217
DB 289 VAAGNSGSDSQTIASPGVSEKVTIVGALDDNTA-----SSDDDTVASFSRGPTVYGKEK 344
QY 218 PDVMAPGTIFLSARSLAPDSF-----WANHDSKYAYMGTSMTATPIVAGNVVAQLREHF 272
DB 345 PDILAPGVNIIILRS-----PNSYIDKLQSSRVGSQYFTMSGTSMATPICAGIAALILQ-- 399
QY 273 VKRGITPK--PSLLKAALIAGAADIGLYPNGNQGWRTLDKSLNV---AYVNESSSL 327
DB 400 -QNPLDTPDEVKELK-----NGTDKW-----KDEDPNIYGAGAVNAENSV 439

RESULT 5
A:Title: Cloning and characterization of the gene for an additional extracellular serine
A:Reference number: A41341; MUID:92041574; PMID:1938892
A:Accession: A41341
A:Molecule type: DNA
A:Residues: 1-806 <SLO>
A:Cross-references: UNIPARC:UPI0000060C20; GB:M76590; NID:g143819; PIDN:
A:Experimental source: strain 168
C:Comment: The amino terminal sequence of the mature protein and a molecular weight of or
C:Genetics:
A:Gene: vpr
A:Start codon: TTG
C:Superfamily: microbial serine proteinase vpr; subtilisin homology
C:Keywords: hydrolase; serine proteinase
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-160/Domain: propeptide #status predicted <PRO>
F:180-548/Domain: subtilisin homology #status atypical <SBT>

Query Match 14.3%; Score 320.5; DB 2; Length 442;
Best Local Similarity 29.7%; Pred. No. 4.4e-13;
Matches 107; Conservative 50; Mismatches 104; Indels 99; Gaps 16;

QY 11 DVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRNTNAN-----D 64
DB 136 EVVRNGQITLGGTVAVVDTGL-----YHPDLEGR-----IGFADWVNQKTEPYD 183
QY 65 TNGHGTAVAGSVLNGSTN-----KGMAPQANLVFOSIMDSGGGLGSLPNSLQTLFSQAVS 120
DB 184 DNGHGTACADVASSGASSGQYRPAEPANLIGVKLVNKQS-GTLDIIIEGV----- 236
QY 121 AGARHTNSWGAENV-----GAYTDSRNVDVVRKND-----MTIL 157
DB 237 -----EWCIOYNEDNPEDIDMSLSLGDALRYDHEQEDPLVRAVEAWSAGIVVC 288
QY 158 FAAGNEGNGGTISAPGTAKNAITVGCATENLRPSFGSYADNINHVAFSSRGPTKDGRIK 217
DB 289 VAAGNSGSDSQTIASPGVSEKVTIVGALDDNTA-----SSDDDTVASFSRGPTVYGKEK 344
QY 218 PDVMAPGTIFLSARSLAPDSF-----WANHDSKYAYMGTSMTATPIVAGNVVAQLREHF 272
DB 345 PDILAPGVNIIILRS-----PNSYIDKLQSSRVGSQYFTMSGTSMATPICAGIAALILQ-- 399
QY 273 VKRGITPK--PSLLKAALIAGAADIGLYPNGNQGWRTLDKSLNV---AYVNESSSL 327
DB 400 -QNPLDTPDEVKELK-----NGTDKW-----KDEDPNIYGAGAVNAENSV 439

RESULT 5
A:Title: Cloning and characterization of the gene for an additional extracellular serine
A:Reference number: A41341; MUID:92041574; PMID:1938892
A:Accession: A41341
A:Molecule type: DNA
A:Residues: 1-806 <SLO>
A:Cross-references: UNIPARC:UPI0000060C20; GB:M76590; NID:g143819; PIDN:
A:Experimental source: strain 168
C:Comment: The amino terminal sequence of the mature protein and a molecular weight of or
C:Genetics:
A:Gene: vpr
A:Start codon: TTG
C:Superfamily: microbial serine proteinase vpr; subtilisin homology
C:Keywords: hydrolase; serine proteinase
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-160/Domain: propeptide #status predicted <PRO>
F:180-548/Domain: subtilisin homology #status atypical <SBT>

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowaka, A.; Seror, A.; Tanakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, A.; Tosato, V.; Uchiyama, K.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: D69730
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-806 <KUN>
A:Cross-references: UNIPARC:UPI0000060C20; GB:Z99123; GB:AL009126; NID:g2636240; PIDN:CAI
A:Experimental source: strain 168
C:Comment: The amino terminal sequence of the mature protein and a molecular weight of or
C:Genetics:
A:Gene: vpr
A:Start codon: TTG
C:Superfamily: microbial serine proteinase vpr; subtilisin homology
C:Keywords: hydrolase; serine proteinase
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-160/Domain: propeptide #status predicted <PRO>
F:180-548/Domain: subtilisin homology #status atypical <SBT>

Query Match 13.8%; Score 310.5; DB 2; Length 806;
Best Local Similarity 23.5%; Pred. No. 4.3e-12;
Matches 129; Conservative 58; Mismatches 157; Indels 205; Gaps 18;

QY 18 GLYGGQIIVAVADTGLDTR-----NDSSMHEAFRGKITALYALGRNTN 60
DB 177 GYTGKGIKVAIIDTVEYNHDPDKNFGQYGDYFVDNDYDPKPTG-----D 225
QY 61 NANDTNGHGTAVAGSVLNGSTNKGMAPOANLVFOSIMDSGGGLGSLPNSLQTLFSQAVS 120
DB 226 PRGEATDGHGTAVAGTAAANG-TIKGVAPDATLLAYRVLGPGG--SGTTENVIAGVERAVQ 282
QY 121 AGARHTNSWGAENVAYTDSRNVDVVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
DB 283 DGADVNNLSLNSLNPNPDWATSTAL-DWAMSEGVAVTISNGSGNGVTVGSPGTSREAI 341
QY 181 TVGATE-----NLRPSFGSY----- 195
DB 342 SVGATQLPLNEVAVTVFGSYSSAKVMGYNKEDDVKALNNKEVELVEAGIGEAKEADFEKOLT 401
QY 196 -----ADNI----- 199
DB 402 GKAVVKGSGIAFVDKADNAXKAGAGIMVYNNLSGEIEANVPGMSVPTIKLSLEDEKEL 461
QY 200 -----NHVAFSSRGPTKD-CRIKPDVMAPGTIFLSARSSSLAP 236
DB 462 VSALKAGETKTKTFLTVSKALGEQVADFSSRGPVNDTWIKPDISAPGVNIVSTIPTHDP 521
QY 237 DSSFWANHDSKYAYMGTSMTATPIVAGNVVAQLREHFVKNRGTTPKPSL--LKAALIAGAA 294
DB 522 D-----HPYGVGSKQGTSMASPHIAGAVAVIKQ-----AKPKWSVEQIKAAIMNTAV 568
QY 295 DI-----GLGYPNGNQGWRTLDKSLNVAYVNESSLSSTSQATYSFTATACKPLKISLV 350
DB 569 TLKOSDGEVYPHNAQAGSARI-----MNAIKADSLVSPGSYSY-----GTFLEK----- 612
QY 351 WSDAPASTTASVTLVNDLVLITAPNGTYQYVNDFTSPVNDNDWG--RNNVENVFVNAQ 408
DB 613 -ENGETNKETFTENQ-----SSIRKSYTLEYFNGSGISISGTSRVRVIPAQ 660
QY 409 SGTVTIEVQ 417
DB 661 TKGATAKVK 669

RESULT 6
A:Title: Cloning and characterization of the gene for an additional extracellular serine
A:Reference number: A41341; MUID:92041574; PMID:1938892
A:Accession: A41341
A:Molecule type: DNA
A:Residues: 1-806 <SLO>
A:Cross-references: UNIPARC:UPI0000060C20; GB:M76590; NID:g143819; PIDN:
A:Experimental source: strain 168
C:Comment: The amino terminal sequence of the mature protein and a molecular weight of or
C:Genetics:
A:Gene: vpr
A:Start codon: TTG
C:Superfamily: microbial serine proteinase vpr; subtilisin homology
C:Keywords: hydrolase; serine proteinase
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-160/Domain: propeptide #status predicted <PRO>
F:180-548/Domain: subtilisin homology #status atypical <SBT>

pyrolysin (EC 3.4.-.-) - *Pyrococcus furiosus*
C:Species: *Pyrococcus furiosus*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T28159

R:Voorhorst, W.G.B.; Eggen, R.I.L.; Geerling, A.C.M.; Platteeuw, C.; Siezen, R.J.; Vos, J. Biol. Chem. 271, 20426-20431, 1996
A:Title: Isolation and characterization of the hyperthermostable serine protease, pyroly
A:Reference number: Z20481; MUID:96355370; PMID:8702780
A:Accession: T28159
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1398 <VOO>
A:Cross-references: UNIPROT:P72186; UNIPARC:UPI000016FD59; EMBL:U55835; NID:g1556462; PI
A:Experimental source: DSM3638
C:Genetics:
A:Gene: pls
C:Keywords: hydrolase; serine proteinase

Query Match 13.5%; Score 302.5; DB 2; Length 1398;
Best Local Similarity 26.6%; Pred. No. 2.9e-11;
Matches 139; Conservative 57; Mismatches 178; Indels 149; Gaps 22;

QY 21 GGGQIVAVADTGLDTRNDSS-----SMHEAFRGKITALLYALGRTNAN----- 63
DB 301 GNGYDIAVDTDLDYDFDVEPLGQYNTYDVAVFSYYYGPLYVLAIEDPNGEYAVFGW 360
QY 64 DTNGHGTAVAGSVLNGSTN-----KGMAPQAN 91
DB 361 DGHGHTVAGTVAGYDSNNDAWMLSMYSGEWEVFSRLYGDYTNVTDTTVQGVAPGAQ 420
QY 92 LVFQSIMDSGGGLGLPSNLQTLPSQAYSAGARIHTNSGNAVNGAYT--TDSRN--VDD 147
DB 421 IMAIRVLRS--DGRGSMWDIIEGM--TYAATHGADVISMISLGG--NAPYLDGTDPSVAVDE 476
QY 148 YVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAITVGATENLRPSGSYAD----- 197
DB 477 LTEKGVVVFVAAGNEGPGINIVSGPVATRAITVGAAA--VPINVGTVSQALGYPDYVG 535
QY 198 -----NINHVAOFSRGPCKGRIPKPDVNAFGTIFLSARSSLAPDSSFWANHDSKYA 249
DB 536 FYFPAITNV--RIAFPSRGPRIIDCEIKPNVAVPGYGIYSSLPMMIGGADF----- 585
QY 250 YMGTSMTPIVAGNVAQLREHFVKNRGITPKPSLLKAALTAGADI-----GLGYPNG 303
DB 586 --MSGTSMTAPHVSGVVALLISG--PKPEGIYVNPDIKKVLESGATWLEGDPYTGQKYTEL 643
QY 304 NQGMGRVTLDKSLNVAIVYNESSLSQTSKATYSFTATAGKPLKISLVMSDAPASTTA--- 360
DB 644 DQGHGLNVTKSWEI-----LKANGTTLPIVDHMAKDSYDFAEYL 685
QY 361 SVTLVNDLDLVITAPN-----GTQYVGN-----DFTSPYNDW-----DG-----RNVENVF 403
DB 686 GVDVIRGLYARNSIPDIVEMHIKYVGDTEYRTFEIYATEPMIKPFVSGSVILENNTEFVL 745
QY 404 -----INAPQSGTY-----TIEVQAYNVVPGQPFS 429
DB 746 RVKYDVEGLEPLGYVGRRIIDPTTPEIIDEILNTIPIPEKT 788

RESULT 7
S11890
serine proteinase (EC 3.4.21.-) precursor, extracellular - Xanthomonas campestris pv. ca
N:Alternate names: subtilisin-related proteinase
C:Species: Xanthomonas campestris pv. campestris
C:Date: 21-Nov-1993 #sequence_revision 07-Feb-1997 #text_change 31-Dec-2004
C:Accession: S11890
R:Liou, Y.N.; Tang, J.L.; Clarke, B.R.; Dow, J.M.; Daniels, M.J.
Mol. Gen. Genet. 220, 433-440, 1990
A:Title: A multipurpose broad host range cloning vector and its use to characterise an e
A:Reference number: S11890; MUID:90251253; PMID:2187155
A:Molecule type: DNA
A:Residues: 1-580 <LIU>
A:Cross-references: UNIPROT:P23314; UNIPARC:UPI000012A398; EMBL:X51635; NID:g48533; PIDN
A:Experimental source: Xanthomonas campestris pv. campestris
A:Note: the sequence from Fig. 4 is inconsistent with that from Fig. 3 in having 205-Ala
C:Superfamily: extracellular alkaline serine protease precursor, Alteromonas type

C:Keywords: extracellular protein; hydrolase; serine proteinase
F:1-32/Domain: signal sequence #status predicted <SIG>
F:168-423/Domain: subtilisin homology <SBT>

Query Match 12.6%; Score 283; DB 2; Length 580;
Best Local Similarity 26.2%; Pred. No. 1.5e-10;
Matches 127; Conservative 55; Mismatches 147; Indels 156; Gaps 24;

QY 21 GGGQIVAVADTGL-----DTGRNDSMHEAFRGKITALLYALGRTNAN----- 64
DB 168 GSGTVVAVIDGITSHADLNANILAGYDFISDAITARDGNGRDSAADEGDWYAANECA 227

QY 65 -----TNGHGTAVAGSVLNGSTNKGMAPOA-----NLVFSQSIMD 99
DB 228 GIPRASSWHGTHVAGTVAAVTNNTTGVAGTAYGAKVVPVRLGKCGGSLSDIADAIVMA 287

QY 100 SGGGLGLPSNLQ--TLFSQAYSAGARIHTNSGNAVNGAYTDSRNVDYVRKNDMTIL 157
DB 288 SGGTVSGIPANANPAEVIINMSLGGGSCSTTMQN--AINGAVSRGT-----TVV 334

QY 158 FAAGNEGPNNGGTISAPGTAKNAITVGATEN--LRPSFGSYADNINHVAQFSSRGPTKDR 215
DB 335 VAAGNDASNVSG--SUPANCANVIAVATTSAGAKASYNFGTI----- 377

QY 216 IKPDVMAFGTIFLSARSS--LAPDSSFWANHDSKYAYMGTSMTAPIVAGNVAQLREHFV 273
DB 378 --DVSAPGSSILTNSGTTTPGS-----ASYASNYGTSMASPHVAGVVALVQS--V 425

QY 274 KNRGITPK--PSLLK--NALIAGAADIGLVPGNGQGRVTLDKSLNVAIVNESS----- 325
DB 426 APTALTTPAAVETLLKNTARALPGAC-----SGCGGAGIVNADAATVAA--INGSGGGG 477

QY 336 -----SLTSOKATYSFTATAGKPLKISLVMSDAPASTTASVTL---VND 367
DB 478 GGGNTLTNGTPTVGLGAATGAEILNVTITVPAG-----SGLTIVTSSGSGD 523

QY 368 LDLVI---TAPNGTQYVGNDFTPSYNDWNGRNNVNFVINAPOSGTGTIEVQAYNVPG 424
DB 534 ADLYVRAGSAPTDSAYT---CRPYRS-----GNAETCTITAP--SGTYVYVRLKAYS----- 569

QY 425 QPTFS 429
DB 570 --TFS 572

RESULT 8

S25835
subtilisin (EC 3.4.21.62) precursor - Bacillus sp. (strain TA41)

C:Species: Bacillus sp.

C:Date: 22-Nov-1993 #sequence_revision 20-Feb-1995 #text_change 05-Oct-2004

C:Accession: S25835

R:Davail, S.; Feller, G.; Narinx, E.; Gerday, C.

Gene 119, 143-144, 1992

A:Title: Sequence of the subtilisin-encoding gene from an antarctic psychrotroph Bacillus

A:Reference number: S25835; MUID:93012966; PMID:1398082

A:Accession: S25835

A:Molecule type: DNA

A:Residues: 1-419 <DAV>

A:Cross-references: UNIPARC:UPI00000BB77A; EMBL:X63533; NID:g40198; PIDN:CAA45096.1; PID:

C:Superfamily: Subtilisin; subtilisin homology

C:Keywords: extracellular protein; hydrolase; serine proteinase

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-110/Domain: propeptide #status predicted <PRO>

F:111-419/Product: microbial serine proteinase #status predicted <MAT>

F:135-373/Domain: subtilisin homology <SBT>

F:144,184,359/Active site: Asp, His, Ser #status predicted

Query Match 12.5%; Score 281; DB 1; Length 419;
Best Local Similarity 33.0%; Pred. No. 1.3e-10;
Matches 87; Conservative 38; Mismatches 97; Indels 42; Gaps 13;

QY 21 GGGQIVAVADTGLDTRNDSSMH--EAFRGKITALLYALGR-----NNANDTNGHGTAVAGSV 76
DB 144,184,359/Active site: Asp, His, Ser #status predicted

Db 135 GAGINIAVLDTGVNTNHPDLSNNVECKD-----FTVGTNFTDNSCTDRQGHGTHVAGSA 189
Qy 77 LQNGSTNK---GMAPQANL-VFQSIWDSGGGLG-GLPSNLQTLFQSYAGARIHTN-SW 130
Db 190 LANGGTGSGVYGVGAPEADLWAYKVLGDGSGYADDAEAI RHAGDQATALTNTKVVINMSL 249
Qy 131 GAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNGGTISAPCTAKNAITVGTATENLRP 190
Db 250 GSGGESSLIT---NAVYAYDKGLVLIIAAGNSGPKPGSIGYGAALNVAVAALENTIQ 306
Qy 191 SFGSYADNINHVAQFSRSGPTKDG-----RIKPDVMAQCTFTLSARSSLAPDSSFWANH 244
Db 307 N-GTY-----RVADFSSRGHKRTAGDYVIQKGDVEISAFGAAYST-----W--F 348
Qy 245 DSKYAVMGTSMATPTVAGNVAOL 268
Db 349 DGGYATISGTSMASPHAAGLAARI 372
RESULT 9
G83753
subtilisin-type proteinase (EC 3.4.21.-) vpr precursor [similarity] - Bacillus haloduran
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: G83753
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: G83753
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-799 <STO>
A:Cross-references: UNIPROT:Q9KEM1; UNIPARC:UPI00000C39DC; GB:AP001510; GB:BA000004; NID
A:Experimental source: strain C-125
C:Genetics:
A:Gene: vpr
C:Superfamily: microbial serine proteinase vpr; subtilisin homology
C:Keywords: hydrolase; serine proteinase
F:1-29/Domain: signal sequence #status predicted <SIG>
Query Match 12.5%; Score 280; DB 2; Length 799;
Best Local Similarity 24.7%; Pred. No. 3.7e-10;
Matches 117; Conservative 50; Mismatches 135; Indels 172; Gaps 16;
Qy 18 GLYGQGIIVAVADTGLDTCGRNDSMHEAFRGKITALYALGRTNANDT-----NGH 68
Db 171 GYTGEITVALDGTVDYTHPD--LVHAF-GDYKGWDFDNDNDPOETPPGDPGRGIETH 227
Qy 69 GTHVAGSVLNGSTNKGMAPQANLVFQSIWDSGGGLGGLPSNLQTLFQSYAGARIHTN 128
Db 228 GTHVAGTVAANGLI-KGVAPDANLLAYRVLGPG--RGSTAGVIAGIERAVQDGADIMNL 284
Qy 129 SNGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNGGTISAPCTAKNAITVGTATENL 188
Db 285 SLGNTLNDPDFATSIAL-DWMAEGVAVTNSNGSGFNNTVGTSGPSTRDAISVGAT---- 340
Qy 189 RPSFGSY-----ADNINH----- 201
Db 341 RLPYNYKASVTSIGIDYPSADIMGFPDSDEHLELDGTYEVAFAGLKPDPGFDVDE 400
Qy 202 ----- 201
Db 401 GKIALIVRGEIPPEKAENAKAAGVAGIYNNVAGVQPTVPGLATPTIMLSNEDGLKMR 460
Qy 202 ----- 201
Db 461 NLENGQNTVTFPIEDKLVGETVADFSSRGPPVMTWIKPDVPSAPGVAIVSTIPTHQPD 520
Qy 238 SSFWANHDSKYAVMGTSMATPTVAGNVAOLREHFVKNRGITPKPSLLKAAIAGAADT- 296
Db 521 DPT-----GYSGRQGTSMASPHVGAALLLEAH-PWNGV-----DHVKAALMNTAENLV 569

Qy 297 ---GLGYPNGNOGGRVTLDKSLNAVYVNESLSLTSQKATV-SFTATAGKPLK 346
Db 570 DENGRIYPHNTQAG-----SIRIVDAIESETLVTPGSHSFGTFTTKERKQVE 617
RESULT 10
T29090
surface layer-associated STABLE proteinase - Staphylothermus marinus
N:Alternate names: hyperthermostable proteinase
C:Species: Staphylothermus marinus
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C:Accession: T29090
R:Mayr, J.; Lupas, A.; Kellermann, J.; Eckerskorn, C.; Baumeister, W.; Peters, J.
Curr. Biol. 6, 739-749, 1996
A:Title: A hyperthermostable protease of the subtilisin family bound to the surface layer
A:Reference number: Z20559; MUID:96385442; PMID:8793300
A:Accession: T29090
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1345 <MAY>
A:Cross-references: UNIPROT:D54437; UNIPARC:UPI0000062778; EMBL:U57968; NID:gl374755; PII
A:Experimental source: strain F1
C:Function:
A:Description: probably serves an exodigestive function related to the organism's energy
A:Note: stoichiometric S-layer component
Query Match 12.4%; Score 279.5; DB 2; Length 1345;
Best Local Similarity 29.9%; Pred. No. 7.9e-10;
Matches 99; Conservative 45; Mismatches 106; Indels 81; Gaps 14;
Qy 46 FRGKITALYALGRTNANDTNGHGHVA-----GSVL-----GNGSTNK-GMAPQANLV 93
Db 445 YQGRYLAL-----VSDFHGHGTSVATVIASRGRLVLDYGDGKLYRIMGVAPGAKI- 495
Qy 94 FQSIWDSGGGLGGLPSNLQTLFQSYAG-----EAWLGFNVTBEEDGVYVLSLDPPFGPHRADIISNW 546
Db 496 -----AGGDAILGNLIVL--EAWLGFNVTBEEDGVYVLSLDPPFGPHRADIISNW 546
Qy 131 GAAVNGAYTTDSRNV-----DYVRKNDMTILFAAGNEGPNGGTISAPGTAK 177
Db 547 GSIYINFMLQPPGIDYRSSFMDEILAIRNYLIGDHVTIVFAAGNEGPGYSSNGAPGTGL 606
Qy 178 NAITVGATE-NLRSPG---SYADNINHVAQFSRSGPTKDGRIKPDVMAQCTFTLSARS 232
Db 607 LVITAGASTLMDYTRIYGYPEGYAD---EVIPFSSRGPTGGQYKPKDINIGAFEWASTR 663
Qy 233 SLAPDSSFWANHDSKYAVMGTSMATPTVAGNVAOLREHFVKNRGITPKPSLLKAAIAG 292
Db 664 TI-DGRGYAQPD----VFGGTSEATPTTSGTIALVFOAYKEVYNTTPDPVTAKIILKSS 718
Qy 293 AADIGLGYPNQNGRVRTLDKSLNAVYVNE 323
Db 719 AKDI--WTPAPSGSGRVDALKAAADTVFISE 747
RESULT 11
S23407
subtilisin (EC 3.4.21.62) 1 precursor - Bacillus sp. (strain TA39)
C:Species: Bacillus sp.
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 05-Oct-2004
C:Accession: S23407
R:Narinx, E.; Davail, S.; Feller, G.; Gerday, C.
Biochim. Biophys. Acta 1131, 111-113, 1992
A:Title: Nucleotide and derived amino acid sequence of the subtilisin from the antarctic
A:Reference number: S23407; MUID:92256481; PMID:1581352
A:Accession: S23407
A:Molecule type: DNA
A:Residues: 1-420 <NAR>
A:Cross-references: UNIPROT:P28842; UNIPARC:UPI0000136183; EMBL:X62369; NID:g40200; PIDN:
C:Genetics:
A:Gene: subI
C:Superfamily: Subtilisin; subtilisin homology
C:Keywords: extracellular protein; hydrolase; serine proteinase

F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-111/Domain: propeptide #status predicted <PRO>
F:112-420/Product: microbial serine proteinase #status predicted <MAT>
F:136-374/Domain: subtilisin homology <SBT>
F:145,185,360/Active site: Asp, His, Ser #status predicted

Query Match 12.3%; Score 277; DB 1; Length 420;
Best Local Similarity 31.2%; Pred. No. 2.4e-10;
Matches 98; Conservative 44; Mismatches 120; Indels 52; Gaps 16;

QY 21 GGGQIVAVADTGLDTRNDSSMHEAFRGKITAL--YALGRT---NNAVDNTHGHGTHVAGS 75
DB 136 GGGINIAVLDTGVNTN-----HPDLNNVEQCKDFTVGTITYNNSCDTRQGHGTHVAGS 189
QY 76 VLNGSTNK--GMAPOANL--VFQSIMDSGGGLG-GLPSNLQTLFQSAVSAGARITHN-S 129
DB 190 ALADGGTGVVGVAPDADLWAYKVLGGDGSYADIDAAAIRHAGDQATALNKTVVINNS 249
QY 130 MGAANGVAYTDSNRVDDTVRRKNDMTILFAAGNEPGNGGTISAPGTAKNAITVGATENLR 189
DB 250 LSSGESSLITNAVN---YSYNGKVLIIAAGNSGPGYQSGIGPGALYNVAVAALEN-K 305
QY 190 PSFGSYADNINIVAFSSRGPT-KDG-----RIKPDVWAPGTFFILSARSSLAPDSSFWAN 243
DB 306 VENGTY-----RVADFSSRGYWTBDYAIQKGDVEISAPGAAYST-----W-- 348
QY 244 HPSKVAYMGTSMATPIVAGNAQLREHFVKRGITPKPSLLKAAALIAAGADIGLGPNG 303
DB 349 FDGGTATISGTSWASPHAGLAAKIAWQYPSASNDVRGELQYRAY---ENDILSGYYAG 405
QY 304 -----NQMGGRVTL 312
DB 406 YGDDFASGFGFATV 419

RESULT 12
JC4908
alkaline serine proteinase (EC 3.4.-.-) I precursor - Alteromonas sp.
N:Alternate names: subtilase
C:Species: Alteromonas sp.
C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 05-Oct-2004
C:Accession: JC4908
R:Tsujiibo, H.; Miyamoto, K.; Tanaka, K.; Kaidzu, Y.; Imada, C.; Okami, Y.; Inamori, Y.
Biosci. Biotechnol. Biochem. 60, 1284-1288, 1996
A:Title: Cloning and sequence analysis of a protease-encoding gene from the marine bacterium *Alteromonas* sp.
A:Reference number: JC4908; MUID:97141200; PMID:8987544
A:Accession: JC4908
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-715 <TSU>
A:Cross-references: UNIPROT:P70765; UNIPARC:UPI000017A928; DDBJ:D38600; NID:g1536787; PI
A:Experimental source: strain O-7
C:Comment: This enzyme belongs to class I subtilisin-like family. It is a chelator-sensit
C:Genetics:
A:Gene: apr1
C:Superfamily: extracellular alkaline serine protease precursor, Alteromonas type
C:Keywords: hydrolase
F:1-40/Domain: signal sequence #status predicted <SIG>
F:41-150/Domain: amino-terminal propeptide #status predicted <ATP>
F:151-496/Product: alkaline serine protease I #status predicted <MAT>
F:182-452/Domain: subtilisin homology <SBT>
F:497-715/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:239-294,335-372,478-481/Disulfide bonds: #status predicted

Query Match 11.9%; Score 267; DB 2; Length 715;
Best Local Similarity 25.9%; Pred. No. 2.1e-09;
Matches 124; Conservative 51; Mismatches 168; Indels 136; Gaps 23;

QY 21 GGGQIVAVADTG-----LDTRNDSSMHEAFRGKITALYALGRNNAND-----TNG---- 67
DB 182 GGGVVAVLDTGYRPHLDLDANILPGYDMISNTFVANDGGARDNDARDPGDAVTRGCT 241
QY 68 -----HGTHVAG---SVLNGSTNKGMAPOANLVFQSIMDSGGGLGLP 108

DB 242 DSSGQVPRADQDSSWHGTHVAGTVAAVTNNGEGVAGVAYDAKVVPVRVL-----GKCGGLT 298
QY 109 SNLQTLFQSAVSAGARIHTNSWGAIV-----NGAYTTDSNRVDDTVYRKNDMTILFAAG 161
DB 299 SDIADGIIWASGSDRVPANANPAVIVNMSLGGGACGATTCQNAIQARNNGTVIVIAAG 358
QY 162 NEGPNGGTISAPGTAKNAITVGAT--ENLRPSPFGSYADNINIHVAQFSRSGPTKDGRIKPD 219
DB 359 NDNDNSANYN-PGNCNGVVNVASVGRDGSRAVYSNYGANI-----D 398
QY 220 VWAPGTFFILSARSSLAPDSSFWANHDS-----KYAYMGTSMATPIVAGNAQLR-- 269
DB 399 VAAPG---GAQSFADDPGEGILSTHNSGSGAPSNDSYHSQGSTMAAPHVAGVAALIKQA 454
QY 270 -----EHFVKN--RGITPKPSLLKAAALIAAGADI--GLG----YPNGNQMGGRVTL 312
DB 455 KPSATPDEVETILKNVTRSPAGSCNCGTGVVDAANAANEALGDVVTPTGN-----TL 508
QY 313 DKSLNVAVNBSSSLTSQKATYSFTATAGKPLKISLVMSDAPASTTASVTL---VNLDLD 369
DB 509 ED--GVAKTGLSGAAGSNQ--PFTFDVPAGK-----TNVTFTMSGGTGDAD 550
QY 370 LVITAPNGTQVGNDFTPSYNDNDGR-----NNVENFINAPQSGTYTIEVQAYNVVPG 424
DB 551 LYVKL--GSQ-----PTSSYDCRPYEGNAEVCSGFDAPQAGTYHVMIINGYKAYS 599

RESULT 13
A72647
probable surface layer-associated STABLE proteinase APE0607 - Aeropyrum pernix (strain KJ
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: A72647
R:Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hailkawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: A72647
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1331 <KAW>
A:Cross-references: UNIPROT:Q9YEG9; UNIPARC:UPI000005DBF6; DDBJ:AP000060; NID:G5104188; I
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE0607

Query Match 11.7%; Score 263; DB 2; Length 1331;
Best Local Similarity 23.6%; Pred. No. 8.8e-09;
Matches 111; Conservative 65; Mismatches 158; Indels 136; Gaps 18;

QY 8 VKADVQSSYGLYGQGOIVAVADTGLDTRNDSSMHE-AFRGKITALYA----- 55
DB 346 VYADLS-TAYLYL-----LKALSDTGMISGEPDPSLLDJSFADETPASYGSEVLARDFTGD 400
QY 56 -----LGRTNNAN-----DTNGH 68
DB 401 GVNDSAGALAGTWYDVWGLLTGESVNLGRWLGFDYAGLVLPGLDPQGRWVSLYDTLAH 460
QY 69 GTHVAGSVLNGSTN-----KGMAPQANLVFQSIMDSGGGLGLGPSNLQTLFQSA 118
DB 461 GTSVATVIASRGVNFNLGYIETSLRGVAPGAKIA-----AGGSP-----LINVFAQL 509
QY 119 YSAG-----ARIHTNSWG-----AAVNGAYT--TDSNRVDDTVVRKNDMT 155
DB 510 FLISGFEPQPSPLNWVYTGHEHQVDVNNNSWGNYSIALRGFLTGADDTATTEDIVSASGTV 569
QY 156 ILFAAGNEPGNGGTISAPGTAKNAITVGATE--NLRPSPFGSYADNINIHVAQFSRSGPTK 213
DB 570 IVHANGNGGPGYGTATTFGAGSLISVGASTLFDYRPFYGLYPSPGGDVLSWSDRGPSQI 629
QY 214 GRIKPDVWAPGTFILSARSSLAPDSSFWANHDSKYAYMGTSMATPIVAGNAQLREHFV 273

Db 630 GVAKPDVNVIGSPAWAG----VPLTGLGNSLAFDIFGTSSEATPTWTSGLVALVISAYQ 685
Qy 274 KRGITPKSLKAAIAGAADIGLGPNGNQGWRTLDKSLNV-----AY 320
Db 686 QAFGAKPSGLVKAILKSTARDTGA--DAFTQSGQVDYVRVAVKAVLEGVPIALSTSVY 743
Qy 321 VNNESSLSQKATYSFTATAGPKLKSILVWSDA--PASTTASVTLVNDL 368
Db 744 ENVYLSLS-----GYSYPLAPNPVEDTQIYPCVLKPGETAETVLVTKL 788
RESULT 14
C84120
subtilisin-type proteinase (EC 3.4.21.-) BH3763 precursor [similarity] - Bacillus halodurans
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: C84120
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: C84120
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-757 <STO>
A:Cross-references: UNIPROT:Q9K6G6; UNIPARC:UPI00000C42C2; GB:AP001519; GB:BA000004; NID
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH3763
C:Superfamily: microbial serine proteinase vpr; subtilisin homology
C:Keywords: hydrolase; serine proteinase
F:1-20/Domain: signal sequence #status predicted <SIG>
Query Match 11.5%; Score 259.5; DB 2; Length 757;
Best Local Similarity 22.6%; Pred. No. 6.8e-09;
Matches 119; Conservative 58; Mismatches 155; Indels 195; Gaps 20;
Qy 8 VKADVAQSSYGLYGQGIIVAVADTGLDGTGRNDSMHEAFRG-----KITALYALG 57
Db 119 VRGMLDEEGVHLTKGVKVAVIDGTIDYTHPD--LQSSYKGGYDFVDYDDPMETIASQG 176
Qy 58 RTNNANDTNGHGHVAGSVLGNSTKMGAPQANLVFQSIMDSGGGLGPSNLQTLFSG 117
Db 177 -----PPTLGRTHVSGIIAANGQV--KGVAPEAIIYVYALGFGG--QQTSEQVIAAIEK 227
Qy 118 AYSAGARIHTNSWGAAGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAK 177
Db 228 AVEDGDVIVNLSLGNVTNGPDPTSLALDAAEVGGVAVT--SNGNSGPNWMTVSGPTSK 286
Qy 178 NAITVGAT-----EN---LRPSFGS----- 194
Db 287 KAISVGASAPLNTPLYTAFGENEISLYPFGSLPWFAPKRDLPMDIVGVGTEKEWEGVD 346
Qy 195 -----YADNINH----- 201
Db 347 ABGKVVLIKRGVMPPEKVMHAAKARGVITNNTPGPTGMIEGGVNIPIVVSITREDG 406
Qy 202 -----VAQFSRGP--TKDGRIKPDVMAPGTIFILSARSS 233
Db 407 EFLLLEQLKQKKELTLRTIYKEEDFVALFSRGPVTHWDKPDVAPGVS-----DS 462
Qy 234 LAPDSFWANHDSKYAVMGGTSMATPIVAGNVAQLREHFVKNRGITPK--PSLLKAAALIA 291
Db 463 TTPNNG-----YLGLNGTSMAPHVAGAAALIKQ-----AHPWTPEQVKAALMN 507
Qy 292 GAADI-----GLGYPNGNQGWRTLDKSLNVAYNVNESSLSQKATYSFTATAGPKLKI 347
Db 508 TAKKLVDQGVGPHIEHQAGRIQVDKAV-----AATSLVYPGALSFGK----- 551
Qy 348 SLVWSDAPASTTASVTL--VNDLDELVITAPNGTQYVGNDFTPSPYNDNW 393
Db 552 ----WSKDDLREKRPVTLTITENHDTV-----KRTYHISPPDPDVGVEW 591

RESULT 15

A35742
aqualysin (EC 3.4.21.-) I precursor - Thermus aquaticus
C:Species: Thermus aquaticus
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C:Accession: A35742; S00620; S00324
R:Terada, I.; Kwon, S.T.; Miyata, Y.; Matsuzawa, H.; Ohta, T.
J. Biol. Chem. 265, 6576-6581, 1990
A:Title: Unique precursor structure of an extracellular protease, aqualysin I, with NH-2-
A:Reference number: A35742; MUID:90216674; PMID:2182621
A:Accession: A35742
A:Molecule type: DNA
A:Residues: 1-513 <TER>
A:Cross-references: UNIPROT:P08594; UNIPARC:UPI0000125D0A; GB:D90108; GB:J054J
A:Note: the authors translated the codon CTG for residue 470 as Val, and GGT for residue
R:Kwon, S.T.; Terada, I.; Matsuzawa, H.; Ohta, T.
Eur. J. Biochem. 173, 491-497, 1988
A:Title: Nucleotide sequence of the gene for aqualysin I (a thermophilic alkaline serine
A:Reference number: S00620; MUID:88225062; PMID:3286255
A:Accession: S00620
A:Molecule type: DNA
A:Residues: 75-442 <KWO>
A:Cross-references: UNIPARC:UPI0000170448; EMBL:X07734; NID:G48069; PIDN:CAA30559.1; PID:
A:Note: part of this sequence, including the amino and carboxyl ends of the mature prote
R:Matsuzawa, H.; Tokugawa, K.; Hamaoki, M.; Mizoguchi, M.; Taguchi, H.; Terada, I.; Kwon,
Eur. J. Biochem. 171, 441-447, 1988
A:Title: Purification and characterization of aqualysin I (a thermophilic alkaline serine
A:Reference number: S00324; MUID:88151937; PMID:3162211
A:Accession: S00324
A:Molecule type: protein
A:Residues: 128-170 <MATS>
A:Cross-references: UNIPARC:UPI0000172C23
C:Superfamily: Subtilisin; subtilisin homology
C:Keywords: extracellular protein; hydrolase; serine proteinase
F:1-14/Domain: signal sequence #status predicted <SIG>
F:15-127/Domain: propeptide #status predicted <PRO>
F:128-408/Product: aqualysin I #status experimental <MAT>
F:157-364/Domain: subtilisin homology <SBT>
F:255-257,281-283/Region: S1 specificity crevice #status predicted
F:409-513/Domain: carboxyl-terminal propeptide #status predicted <CPR>
F:166,197,349/Active site: Asp, His, Ser #status predicted
Query Match 11.5%; Score 257.5; DB 1; Length 513;
Best Local Similarity 26.0%; Pred. No. 5.4e-09;
Matches 117; Conservative 44; Mismatches 144; Indels 145; Gaps 23;
Qy 16 SYGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALY-ALGRTNANDTNGHGHVAG 74
Db 152 TTTATGRGVNVVVIDTGIRT-----THREFGRARVGYDALG--GNGQDCNHGHVAG 203
Qy 75 SYLGNSTKMGAPQANLVFQSIMD--SGGLGLGPSNLQTLFSQAYSAGARIHTN---- 128
Db 204 TI---GGVYGVAKAVNLVAVRVLDNCGSGSGTSVGIAGVDV-----TNHRRPAVA 252
Qy 129 --SWGAANGVAYTTDSRNVDYVRKN---DMTILFAAGNEGNGGTISAPGTAKNAITVG 183
Db 253 NMSLGGGVSTA-----LDNAVKNLSAAGVVVVAAGNDNANACNYS--PARVAEALTVG 304
Qy 184 AT--ENLRPSFGSYADNHNHVAQFSRGPDKGRKPDVMAAGTIFILSARSLAPDSSF 241
Db 305 ATTSDARASFSNYSQV-----DLFAPGASIPSA-----W 335
Qy 242 ANHDSKYAVMGGTSMATPIVAGNVAQLREHFVKNRGITP---KPSLLKAAIAGADIGL 298
Db 336 YTSDTATQTLNGTSWATPHVAG--VAAL---YLEQNPSTPASVASAILNGATTGRLSGIGS 392
Qy 299 GYPNGNQGWRTLDKSLNVAYNVNESSLSQKATYSFTATAGPKLKSILVWSDAPAST 358
Db 393 GSPN-----RLLYSLSSGS-----GSTAPCT 415
Qy 359 ----TASVTLVNDLDELVITAPNGTQY-----VGNDFTPSYNDWNDCRN---- 397

Db 416 CSYTGSLSGPDYNF---QPNGTYYSFAGTHRAWLRGPACTDF-DLYLWMDGSRWLT 471
QY 398 -----NVENVFINAPQSGTYTIEVQAYN 420
Db 472 VGSSTGPTSEESLSYSTAGTYLWRIYAYS 501

Search completed: April 7, 2006, 09:43:27
Job time : 42 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 7, 2006, 09:41:20 ; Search time 82 Seconds
(without alignments)
2211.438 Million cell updates/sec

Title: US-10-820-714A-1

Perfect score: 2247

Sequence: 1 NDVARGIKADVQAQSSVGLV.....EVQAYNVPGPQTFLAIYN 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2247	100.0	434	3	US-09-985-689A-1
2	2247	100.0	434	4	US-10-385-662-2
3	2247	100.0	434	4	US-10-456-479-2
4	2247	100.0	434	4	US-10-837-566-1
5	2247	100.0	434	5	US-10-820-712A-1
6	2247	100.0	434	5	US-10-820-714A-1
7	2247	100.0	640	3	US-09-920-954-6
8	2247	100.0	640	4	US-10-456-479-4
9	2247	100.0	640	4	US-10-784-870-6
10	2247	100.0	640	5	US-10-820-712A-3
11	2247	100.0	640	5	US-10-820-714A-3
12	2242	99.8	434	4	US-10-456-479-11
13	2242	99.8	434	5	US-10-820-712A-14
14	2242	99.8	434	5	US-10-820-714A-15
15	2242	99.8	640	3	US-09-920-954-8
16	2242	99.8	640	4	US-10-784-870-8
17	2191	97.5	434	3	US-09-985-689A-2
18	2191	97.5	434	4	US-10-456-479-10
19	2191	97.5	434	4	US-10-837-566-2
20	2191	97.5	434	5	US-10-820-712A-12
21	2191	97.5	434	5	US-10-820-714A-13
22	2183	97.2	639	3	US-09-920-954-4
23	2183	97.2	639	4	US-10-784-870-4
24	2155	95.9	639	3	US-09-920-954-1
25	2155	95.9	639	4	US-10-784-870-1
26	2155	95.9	640	3	US-09-920-954-2
27	2155	95.9	640	4	US-10-784-870-2

28	2143	95.4	434	3	US-09-985-689A-6	Sequence 6, Appli
29	2143	95.4	434	4	US-10-456-479-15	Sequence 15, Appl
30	2143	95.4	434	4	US-10-837-566-6	Sequence 6, Appli
31	2143	95.4	434	5	US-10-820-712A-22	Sequence 22, Appl
32	2143	95.4	434	5	US-10-820-714A-23	Sequence 23, Appl
33	2125.5	94.6	433	3	US-09-985-689A-7	Sequence 7, Appli
34	2125.5	94.6	433	4	US-10-456-479-16	Sequence 16, Appl
35	2125.5	94.6	433	4	US-10-837-566-7	Sequence 7, Appli
36	2125.5	94.6	433	5	US-10-820-712A-23	Sequence 23, Appl
37	2125.5	94.6	433	5	US-10-820-714A-24	Sequence 24, Appl
38	1998.5	88.9	433	3	US-09-985-689A-5	Sequence 5, Appli
39	1998.5	88.9	433	4	US-10-456-479-14	Sequence 14, Appl
40	1998.5	88.9	433	4	US-10-837-566-5	Sequence 5, Appli
41	1998.5	88.9	433	5	US-10-820-712A-20	Sequence 20, Appl
42	1998.5	88.9	433	5	US-10-820-714A-21	Sequence 21, Appl
43	1994.5	88.8	433	3	US-09-985-689A-3	Sequence 3, Appli
44	1994.5	88.8	433	4	US-10-456-479-12	Sequence 12, Appl
45	1994.5	88.8	433	4	US-10-837-566-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-985-689A-1
; Sequence 1, Application US/09985689A
; Publication No. US20030022351A1
; GENERAL INFORMATION:
; APPLICANT: HATADA, YUJI
; APPLICANT: OGAWA, AKINORI
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHISA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483US0
; CURRENT APPLICATION NUMBER: US/09/985,689A
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-985-689A-1

Query Match						100.0%; Score 2247; DB 3; Length 434;
Best Local Similarity						100.0%; Pred. No. 3.6e-171; Mismatches 0; Indels 0; Gaps 0;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1	NDVARGIKADVQAQSSVGLYGQGI	VAVADTGLDTRNDSSMHEAFRGKIT	YALGRTN	60	
DB	1	NDVARGIKADVQAQSSVGLYGQGI	VAVADTGLDTRNDSSMHEAFRGKIT	YALGRTN	60	
QY	61	NANDTNGHGT	HVAGSVLNGSTNKGMAQANLVFOS	IMDSGGGLGGLPSNLQTLFSQAYS	120	
DB	61	NANDTNGHGT	HVAGSVLNGSTNKGMAQANLVFOS	IMDSGGGLGGLPSNLQTLFSQAYS	120	
QY	121	AGARHTNSGAAVNGAYTTDSRNVD	VTFRKNDMTILFAAGNEGNGGT	ISAPGTAKNAI	180	
DB	121	AGARHTNSGAAVNGAYTTDSRNVD	VTFRKNDMTILFAAGNEGNGGT	ISAPGTAKNAI	180	
QY	181	TVGATENLRPSFGSYADNIN	HAQFSSRGPTKDGRIKPDVMA	PGTFILSRSSSLAPDSSF	240	
DB	181	TVGATENLRPSFGSYADNIN	HAQFSSRGPTKDGRIKPDVMA	PGTFILSRSSSLAPDSSF	240	
QY	241	WANHDSKYVMGGTSMATPI	VAGNVAQUREHFVKNRGITP	KPSLLKAAIAGAADIGLY	300	

us-10-820-714a-1.rapbm

Mon Apr 10 06:49:18 2006

QY 301 PNGNQGWGRTVLDKSLNVAAYVNESSLSSTQKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 301 PNGNQGWGRTVLDKSLNVAAYVNESSLSSTQKATYSFTATAGKPLKISLVWSDAPASTTA 360
QY 361 SVTLVNDLVLVITAPNGTQYVGNDFTSYNDNDWGRNNVENVFINAPQSGTYTIEVOAYN 420
Db 361 SVTLVNDLVLVITAPNGTQYVGNDFTSYNDNDWGRNNVENVFINAPQSGTYTIEVOAYN 420
QY 421 VPVGPQTFSLAIVN 434
Db 421 VPVGPQTFSLAIVN 434

RESULT 3
US-10-456-479-2
; Sequence 2, Application US/10456479
; Publication No. US2004007232A1
; GENERAL INFORMATION:
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: TAKIMURA, YASUSHI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: NOMURA, MASAFUMI
; APPLICANT: KOBAYASHI, TORRU
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 238700USO
; CURRENT APPLICATION NUMBER: US/10/456,479
; CURRENT FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: JP 2002-186387
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: JP 2002-304232
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-456-479-2

Query Match 100.0%; Score 2247; DB 4; Length 434;
Best Local Similarity 100.0%; Pred. No. 3.6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVQSSYGLYGQGIIVADVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVQSSYGLYGQGIIVADVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARIHTNSWGAANVANGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSWGAANVANGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPOGTFILSARSLAPDSSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPOGTFILSARSLAPDSSF 240
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300
Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300
QY 301 PNGNQGWGRTVLDKSLNVAAYVNESSLSSTQKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 301 PNGNQGWGRTVLDKSLNVAAYVNESSLSSTQKATYSFTATAGKPLKISLVWSDAPASTTA 360
QY 361 SVTLVNDLVLVITAPNGTQYVGNDFTSYNDNDWGRNNVENVFINAPQSGTYTIEVOAYN 420
Db 361 SVTLVNDLVLVITAPNGTQYVGNDFTSYNDNDWGRNNVENVFINAPQSGTYTIEVOAYN 420
QY 421 VPVGPQTFSLAIVN 434

Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300
QY 301 PNGNQGWGRTVLDKSLNVAAYVNESSLSSTQKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 301 PNGNQGWGRTVLDKSLNVAAYVNESSLSSTQKATYSFTATAGKPLKISLVWSDAPASTTA 360
QY 361 SVTLVNDLVLVITAPNGTQYVGNDFTSYNDNDWGRNNVENVFINAPQSGTYTIEVOAYN 420
Db 361 SVTLVNDLVLVITAPNGTQYVGNDFTSYNDNDWGRNNVENVFINAPQSGTYTIEVOAYN 420
QY 421 VPVGPQTFSLAIVN 434
Db 421 VPVGPQTFSLAIVN 434

RESULT 2
US-10-385-662-2
; Sequence 2, Application US/10385662
; Publication No. US20040002432A1
; GENERAL INFORMATION:
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: SAITO, KAZUHIRO
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: IZAWA, YOSHIFUMI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KOBAYASHI, TORRU
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: Alkaline protease
; FILE REFERENCE: 234938USO
; CURRENT APPLICATION NUMBER: US/10/385,662
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: JP 2002-081428
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: JP 2002-165987
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: JP 2002-304230
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: JP 2002-304231
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-385-662-2

Query Match 100.0%; Score 2247; DB 4; Length 434;
Best Local Similarity 100.0%; Pred. No. 3.6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVQSSYGLYGQGIIVADVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVQSSYGLYGQGIIVADVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARIHTNSWGAANVANGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSWGAANVANGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPOGTFILSARSLAPDSSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPOGTFILSARSLAPDSSF 240
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300
Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADIGLY 300


```
Db 421 VPVGPQTFLSLAIN 434
|||||
RESULT 4
US-10-837-566-1
; Sequence 1, Application US/10837566
; Publication No. US20040203129A1
; GENERAL INFORMATION:
; APPLICANT: HATADA, YUJI
; APPLICANT: OGAWA, AKINORI
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSURISA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483USO
; CURRENT APPLICATION NUMBER: US/10/837,566
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: US/09/985,689A
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-837-566-1

Query Match 100.0%; Score 2247; DB 4; Length 434;
Best Local Similarity 100.0%; Pred. No. 3.6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAAQSSVGLYGQGIIVAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAAQSSVGLYGQGIIVAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60
Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Qy 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGTTISAPGTAKNAI 180
Db 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGTTISAPGTAKNAI 180
Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFLSARSSLAPDSSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFLSARSSLAPDSSF 240
Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALAGAADIGLY 300
Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALAGAADIGLY 300
Qy 301 PNGNOGWRVTLDKSLNVAAYVNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 301 PNGNOGWRVTLDKSLNVAAYVNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 360
Qy 361 SVTLVNDLVLVITAPNGTQVGNDFTSFYNDNDGRNNVENFINAPQSGTYYTIEVOAYN 420
Db 361 SVTLVNDLVLVITAPNGTQVGNDFTSFYNDNDGRNNVENFINAPQSGTYYTIEVOAYN 420
Qy 421 VPVGPQTFLSLAIN 434
Db 421 VPVGPQTFLSLAIN 434

RESULT 5
US-10-820-714a-1
; Sequence 1, Application US/10820714A
; Publication No. US20050214922A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuyoshi
; APPLICANT: Izawa, Yoshifumi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Koyama, Shingo
; APPLICANT: Sato, Tsuyoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251701-USO
; CURRENT APPLICATION NUMBER: US/10/820,712A
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 2003-106708
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-820-712A-1

Query Match 100.0%; Score 2247; DB 5; Length 434;
Best Local Similarity 100.0%; Pred. No. 3.6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAAQSSVGLYGQGIIVAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAAQSSVGLYGQGIIVAVADTGLDTGRNDSMHEAFRGKITALYALGRTN 60
Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Qy 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGTTISAPGTAKNAI 180
Db 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGTTISAPGTAKNAI 180
Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFLSARSSLAPDSSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFLSARSSLAPDSSF 240
Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALAGAADIGLY 300
Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAAALAGAADIGLY 300
Qy 301 PNGNOGWRVTLDKSLNVAAYVNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 301 PNGNOGWRVTLDKSLNVAAYVNESSLSSTQKATYSFTATAGKPLKISLVMSDAPASTTA 360
Qy 361 SVTLVNDLVLVITAPNGTQVGNDFTSFYNDNDGRNNVENFINAPQSGTYYTIEVOAYN 420
Db 361 SVTLVNDLVLVITAPNGTQVGNDFTSFYNDNDGRNNVENFINAPQSGTYYTIEVOAYN 420
Qy 421 VPVGPQTFLSLAIN 434
Db 421 VPVGPQTFLSLAIN 434

RESULT 6
US-10-820-714a-1
; Sequence 1, Application US/10820714A
; Publication No. US20050214922A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuyoshi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Sumitomo, Nobuyuki
; APPLICANT: Takimura, Yasushi
; APPLICANT: Sato, Tsuyoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
```

; FILE REFERENCE: 251697US0			; NUMBER OF SEQ ID NOS: 24		
; CURRENT APPLICATION NUMBER: US/10/820,714A			; SOFTWARE: PatentIn version 3.0		
; CURRENT FILING DATE: 2004-04-09			; SEQ ID NO 6		
; PRIOR APPLICATION NUMBER: 2003-106709			; LENGTH: 640		
; PRIOR FILING DATE: 2003-04-10			; TYPE: PRT		
; NUMBER OF SEQ ID NOS: 24			; ORGANISM: Bacillus sp.		
; SOFTWARE: PatentIn version 3.2			US-09-920-954-6		
; SEQ ID NO 1			Query Match		
; LENGTH: 434			Best Local Similarity 100.0%; Score 2247; DB 5; Length 434;		
; TYPE: PRT			Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
; ORGANISM: Bacillus sp. KSM-KP43					
US-10-820-714A-1					
QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAPRGKITALYALGRTN 60			QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAPRGKITALYALGRTN 60		
DB 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAPRGKITALYALGRTN 60			DB 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAPRGKITALYALGRTN 266		
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120			QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120		
DB 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120			DB 267 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 326		
QY 121 AGARIHTNSWGAANGAYTTDSRNVDYVVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180			QY 121 AGARIHTNSWGAANGAYTTDSRNVDYVVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180		
DB 121 AGARIHTNSWGAANGAYTTDSRNVDYVVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180			DB 327 AGARIHTNSWGAANGAYTTDSRNVDYVVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 386		
QY 181 TVGATENLRPSFGSYADNINHVAQFSRGTGDKRIKPDVMAPTGTFILSARSLAPDSSF 240			QY 181 TVGATENLRPSFGSYADNINHVAQFSRGTGDKRIKPDVMAPTGTFILSARSLAPDSSF 240		
DB 181 TVGATENLRPSFGSYADNINHVAQFSRGTGDKRIKPDVMAPTGTFILSARSLAPDSSF 240			DB 387 TVGATENLRPSFGSYADNINHVAQFSRGTGDKRIKPDVMAPTGTFILSARSLAPDSSF 446		
QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNGRGIITPKPSLLKAALIAGAADIGLGY 300			QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNGRGIITPKPSLLKAALIAGAADIGLGY 300		
DB 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNGRGIITPKPSLLKAALIAGAADIGLGY 300			DB 447 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNGRGIITPKPSLLKAALIAGAADIGLGY 506		
QY 301 PNGNQGWGRVTLDKSLNVAIVYNESSLSQKATYSFTATAGKPLKISLVWSDAPASTTA 360			QY 301 PNGNQGWGRVTLDKSLNVAIVYNESSLSQKATYSFTATAGKPLKISLVWSDAPASTTA 360		
DB 301 PNGNQGWGRVTLDKSLNVAIVYNESSLSQKATYSFTATAGKPLKISLVWSDAPASTTA 360			DB 507 PNGNQGWGRVTLDKSLNVAIVYNESSLSQKATYSFTATAGKPLKISLVWSDAPASTTA 566		
QY 361 SVTLVNDLVLITAPNGTOYVGNDFTPYNDNWDGRNNVFNAPQSGTYYTIEVOAYN 420			QY 361 SVTLVNDLVLITAPNGTOYVGNDFTPYNDNWDGRNNVFNAPQSGTYYTIEVOAYN 420		
DB 361 SVTLVNDLVLITAPNGTOYVGNDFTPYNDNWDGRNNVFNAPQSGTYYTIEVOAYN 420			DB 567 SVTLVNDLVLITAPNGTOYVGNDFTPYNDNWDGRNNVFNAPQSGTYYTIEVOAYN 626		
QY 421 VPVGPQTFFSLAIVN 434			QY 421 VPVGPQTFFSLAIVN 434		
DB 421 VPVGPQTFFSLAIVN 434			DB 627 VPVGPQTFFSLAIVN 640		
RESULT 7			RESULT 8		
US-09-920-954-6			US-10-456-479-4		
; Sequence 6, Application US/09920954			; Sequence 4, Application US/10456479		
; Publication No. US20020064854A1			; Publication No. US20040072321A1		
; GENERAL INFORMATION:			; GENERAL INFORMATION:		
; APPLICANT: TAKAIWA, MIKIO			; APPLICANT: SATO, TSUYOSHI		
; APPLICANT: OKUDA, MITSUYOSHI			; APPLICANT: OKUDA, MITSUYOSHI		
; APPLICANT: SAEKI, KATSUHISA			; APPLICANT: TAKIMURA, YASUSHI		
; APPLICANT: KUBOTA, HIROMI			; APPLICANT: SUMITOMO, NOBUYUKI		
; APPLICANT: HITOMI, JUN			; APPLICANT: NOMURA, MASAFUMI		
; APPLICANT: KAGEYAMA, YASUSHI			; APPLICANT: KOBAYASHI, TOHRU		
; APPLICANT: SHIKATA, SHITSUO			; TITLE OF INVENTION: ALKALINE PROTEASE		
; APPLICANT: NOMURA, MASAFUMI			; FILE REFERENCE: 2387000U50		
; TITLE OF INVENTION: ALKALINE PROTEASE			; CURRENT APPLICATION NUMBER: US/10/456,479		
; FILE REFERENCE: 0327-0832-0PCT			; CURRENT FILING DATE: 2003-06-09		
; CURRENT APPLICATION NUMBER: US/09/920,954			; PRIOR APPLICATION NUMBER: JP 2002-186387		
; CURRENT FILING DATE: 2001-08-03			; PRIOR FILING DATE: 2002-06-26		
; PRIOR APPLICATION NUMBER: 09/509,814			; PRIOR APPLICATION NUMBER: JP 2002-304232		
; PRIOR FILING DATE: 2000-04-06			; PRIOR FILING DATE: 2002-10-18		
; PRIOR APPLICATION NUMBER: PCT/JF98/04528			; NUMBER OF SEQ ID NOS: 16		
; PRIOR FILING DATE: 1998-10-07			; SOFTWARE: PatentIn version 3.1		
; PRIOR APPLICATION NUMBER: JP 9-274570			; SEQ ID NO 4		
; PRIOR FILING DATE: 1997-06-08			; LENGTH: 640		
			; TYPE: PRT		
			; ORGANISM: Bacillus sp. KSM-KP43		
			US-10-456-479-4		
Query Match			Query Match		
100.0%; Score 2247; DB 4; Length 640;			100.0%; Score 2247; DB 4; Length 640;		

```
Best Local Similarity 100.0%; Pred. No. 6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAPRGKITALYALGRTN 60
    |||||
Db 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAPRGKITALYALGRTN 266
    |||||
QY 61 NANTDNGHGTTHVAGSVLGNSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
    |||||
Db 267 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAPRGKITALYALGRTN 266
    |||||
QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
    |||||
Db 267 NANTDNGHGTTHVAGSVLGNSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
    |||||
QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
    |||||
Db 327 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 386
    |||||
QY 181 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPGTFILSARSLAPDSSF 240
    |||||
Db 327 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 386
    |||||
QY 181 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPGTFILSARSLAPDSSF 240
    |||||
Db 387 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPGTFILSARSLAPDSSF 446
    |||||
QY 241 WANHDSKYAYMGSTSMATPIVAGNVAQLREHFVKRGTTPKPSLLKAALIAGAADIIGLY 300
    |||||
Db 447 WANHDSKYAYMGSTSMATPIVAGNVAQLREHFVKRGTTPKPSLLKAALIAGAADIIGLY 506
    |||||
QY 301 PNGNCGWRVTLDKSLNVAYNNESSLSSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
    |||||
Db 507 PNGNCGWRVTLDKSLNVAYNNESSLSSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 566
    |||||
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNWDGRNNVENVFINAPQSGTYTIEVQAYN 420
    |||||
Db 567 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNWDGRNNVENVFINAPQSGTYTIEVQAYN 626
    |||||
QY 421 VPVGPQTFSLAIVN 434
    |||||
Db 627 VPVGPQTFSLAIVN 640
    |||||

RESULT 9
US-10-784-870-6
; Sequence 6, Application US/10784870
; Publication No. US20040142837A1
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUMI
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT APPLICATION NUMBER: US/10/784,870
; CURRENT FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: US/09/509,814A
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-784-870-6

Query Match 100.0%; Score 2247; DB 4; Length 640;
Best Local Similarity 100.0%; Pred. No. 6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAPRGKITALYALGRTN 60
    |||||
```

```
Db 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAPRGKITALYALGRTN 266
    |||||
QY 61 NANTDNGHGTTHVAGSVLGNSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
    |||||
Db 267 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAPRGKITALYALGRTN 266
    |||||
QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
    |||||
Db 327 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 386
    |||||
QY 181 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPGTFILSARSLAPDSSF 240
    |||||
Db 387 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPGTFILSARSLAPDSSF 446
    |||||
QY 241 WANHDSKYAYMGSTSMATPIVAGNVAQLREHFVKRGTTPKPSLLKAALIAGAADIIGLY 300
    |||||
Db 447 WANHDSKYAYMGSTSMATPIVAGNVAQLREHFVKRGTTPKPSLLKAALIAGAADIIGLY 506
    |||||
QY 301 PNGNCGWRVTLDKSLNVAYNNESSLSSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
    |||||
Db 507 PNGNCGWRVTLDKSLNVAYNNESSLSSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 566
    |||||
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNWDGRNNVENVFINAPQSGTYTIEVQAYN 420
    |||||
Db 567 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNWDGRNNVENVFINAPQSGTYTIEVQAYN 626
    |||||
QY 421 VPVGPQTFSLAIVN 434
    |||||
Db 627 VPVGPQTFSLAIVN 640
    |||||

RESULT 10
US-10-820-712A-3
; Sequence 3, Application US/10820712A
; Publication No. US20050026804A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuoyoshi
; APPLICANT: Izawa, Yoshifumi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Koyama, Shingo
; APPLICANT: Sato, Tsuyoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251701-US0
; CURRENT APPLICATION NUMBER: US/10/820,712A
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 2003-106708
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-820-712A-3

Query Match 100.0%; Score 2247; DB 5; Length 640;
Best Local Similarity 100.0%; Pred. No. 6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAPRGKITALYALGRTN 60
    |||||
Db 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAPRGKITALYALGRTN 266
    |||||
QY 61 NANTDNGHGTTHVAGSVLGNSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
    |||||
Db 267 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAPRGKITALYALGRTN 266
    |||||
QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
    |||||
Db 327 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 386
    |||||
QY 181 TVGATENLRPSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPGTFILSARSLAPDSSF 240
    |||||
```

|||||
387 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAFGTFLSARSSLAPOSSF 446
QY 241 WANHDSKYAYMGTSMATPIVAGNVAQIAREHFVKRGITPKPSLLKAALIAGAADIGLY 300
Db 447 WANHDSKYAYMGTSMATPIVAGNVAQIAREHFVKRGITPKPSLLKAALIAGAADIGLY 506
QY 301 PNGNOGWRVTLDKSLNAVYVNESSLSTSKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 507 PNGNOGWRVTLDKSLNAVYVNESSLSTSKATYSFTATAGKPLKISLVMSDAPASTTA 566
QY 361 SVTLVNDLDLVTAPNGTQYVGNDFTSYNDNDWGRNNVNFVFNAPQSGTYTIEVQAYN 420
Db 567 SVTLVNDLDLVTAPNGTQYVGNDFTSYNDNDWGRNNVNFVFNAPQSGTYTIEVQAYN 626
QY 421 VPVGPQTFSLAIVN 434
Db 627 VPVGPQTFSLAIVN 640
RESULT 11
US-10-820-714A-3
; Sequence 3, Application US/10820714A
; Publication No. US20050214922A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuyoshi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Sumitomo, Nobuyuki
; APPLICANT: Takimura, Yasuhide
; APPLICANT: Sato, Tsuyoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251697US0
; CURRENT APPLICATION NUMBER: US/10/820,714A
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 2003-106709
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 3
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-820-714A-3

Query Match 100.0%; Score 2247; DB 5; Length 640;
Best Local Similarity 100.0%; Pred. No. 6e-171;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 266
QY 61 NANDTNGHGTAVAGSVLNGSTNKGMAPOANLVFOSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 267 NANDTNGHGTAVAGSVLNGSTNKGMAPOANLVFOSIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
Db 327 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 386
QY 181 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAFGTFLSARSSLAPOSSF 240
Db 387 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAFGTFLSARSSLAPOSSF 446
QY 241 WANHDSKYAYMGTSMATPIVAGNVAQIAREHFVKRGITPKPSLLKAALIAGAADIGLY 300
Db 447 WANHDSKYAYMGTSMATPIVAGNVAQIAREHFVKRGITPKPSLLKAALIAGAADIGLY 506
QY 301 PNGNOGWRVTLDKSLNAVYVNESSLSTSKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 507 PNGNOGWRVTLDKSLNAVYVNESSLSTSKATYSFTATAGKPLKISLVMSDAPASTTA 566

QY 361 SVTLVNDLDLVTAPNGTQYVGNDFTSYNDNDWGRNNVNFVFNAPQSGTYTIEVQAYN 420
Db 567 SVTLVNDLDLVTAPNGTQYVGNDFTSYNDNDWGRNNVNFVFNAPQSGTYTIEVQAYN 626
QY 421 VPVGPQTFSLAIVN 434
Db 627 VPVGPQTFSLAIVN 640
RESULT 12
US-10-456-479-11
; Sequence 11, Application US/10456479
; Publication No. US20040072321A1
; GENERAL INFORMATION:
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: TAKIMURA, YASUSHI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: NOMURA, MASAFUMI
; APPLICANT: KOBAYASHI, TOHRU
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 238700US0
; CURRENT APPLICATION NUMBER: US/10/456,479
; CURRENT FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: JP 2002-186387
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: JP 2002-304232
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 11
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP9865
US-10-456-479-11

Query Match 99.8%; Score 2242; DB 4; Length 434;
Best Local Similarity 99.8%; Pred. No. 9e-171;
Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNGHGTAVAGSVLNGSTNKGMAPOANLVFOSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NANDTNGHGTAVAGSVLNGSTNKGMAPOANLVFOSIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAFGTFLSARSSLAPOSSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQSSRGPTKDGRIKPDVMAFGTFLSARSSLAPOSSF 240
QY 241 WANHDSKYAYMGTSMATPIVAGNVAQIAREHFVKRGITPKPSLLKAALIAGAADIGLY 300
Db 241 WANHDSKYAYMGTSMATPIVAGNVAQIAREHFVKRGITPKPSLLKAALIAGAADIGLY 300
QY 301 PNGNOGWRVTLDKSLNAVYVNESSLSTSKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 301 PNGNOGWRVTLDKSLNAVYVNESSLSTSKATYSFTATAGKPLKISLVMSDAPASTTA 360
QY 361 SVTLVNDLDLVTAPNGTQYVGNDFTSYNDNDWGRNNVNFVFNAPQSGTYTIEVQAYN 420
Db 361 SVTLVNDLDLVTAPNGTQYVGNDFTSYNDNDWGRNNVNFVFNAPQSGTYTIEVQAYN 420
QY 421 VPVGPQTFSLAIVN 434
Db 421 VPVGPQTFSLAIVN 434

RESULT 13

US-10-820-712A-14
; Sequence 14, Application US/10820712A
; Publication No. US20050026804A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuyoshi
; APPLICANT: Izawa, Yoshifumi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Koyama, Shingo
; APPLICANT: Sato, Tsuyoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251701-USO
; CURRENT APPLICATION NUMBER: US/10/820,712A
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 2003-106708
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-9865
US-10-820-712A-14

Query Match 99.8%; Score 2242; DB 5; Length 434;
Best Local Similarity 99.8%; Pred. No. 9e-171;
Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGI VAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB 1 NDVARGIVKADVAQSSYGLYGQGI VAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60

QY 61 NANDTNGHGTHTVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGSLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGTHTVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGSLPSNLQTLFSQAYS 120

QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
DB 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180

QY 181 TVGATENLRPSFGSVADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLPDSSF 240
DB 181 TVGATENLRPSFGSVADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLPDSSF 240

QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
DB 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300

QY 301 PNGNQGWGRVTLDKSLNVAYNNESSLSSTSKATYSFTATAGKPLKISLVWSDAPASTTA 360
DB 301 PNGNQGWGRVTLDKSLNVAYNNESSLSSTSKATYSFTATAGKPLKISLVWSDAPASTTA 360

QY 361 SVTLVNDLDLVITAPNGTQYVGNDFTPSYNNWDRNNVNFVINAPOSQTYTIEVQAYN 420
DB 361 SVTLVNDLDLVITAPNGTQYVGNDFTPSYNNWDRNNVNFVINAPOSQTYTIEVQAYN 420

QY 421 VPVGPQTFSLAIVN 434
DB 421 VPVGPQTFSLAIVN 434

RESULT 14

US-10-820-714A-15
; Sequence 15, Application US/10820714A
; Publication No. US20050214922A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuyoshi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Sumitomo, Nobuyuki
; APPLICANT: Takimura, Yasuehi
; APPLICANT: Sato, Tsuyoshi

; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251697USO
; CURRENT APPLICATION NUMBER: US/10/820,714A
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 2003-106709
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-9865
US-10-820-714A-15

Query Match 99.8%; Score 2242; DB 5; Length 434;
Best Local Similarity 99.8%; Pred. No. 9e-171;
Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGI VAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB 1 NDVARGIVKADVAQSSYGLYGQGI VAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60

QY 61 NANDTNGHGTHTVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGSLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGTHTVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGSLPSNLQTLFSQAYS 120

QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
DB 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180

QY 181 TVGATENLRPSFGSVADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLPDSSF 240
DB 181 TVGATENLRPSFGSVADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLPDSSF 240

QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
DB 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300

QY 301 PNGNQGWGRVTLDKSLNVAYNNESSLSSTSKATYSFTATAGKPLKISLVWSDAPASTTA 360
DB 301 PNGNQGWGRVTLDKSLNVAYNNESSLSSTSKATYSFTATAGKPLKISLVWSDAPASTTA 360

QY 361 SVTLVNDLDLVITAPNGTQYVGNDFTPSYNNWDRNNVNFVINAPOSQTYTIEVQAYN 420
DB 361 SVTLVNDLDLVITAPNGTQYVGNDFTPSYNNWDRNNVNFVINAPOSQTYTIEVQAYN 420

QY 421 VPVGPQTFSLAIVN 434
DB 421 VPVGPQTFSLAIVN 434

RESULT 15

US-09-920-954-8
; Sequence 8, Application US/09920954
; Publication No. US20020064854A1
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUW
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-0PCT
; CURRENT APPLICATION NUMBER: US/09/920,954
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/509,814
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570

```
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-920-954-8

Query Match      99.8%; Score 2242; DB 3; Length 640;
Best Local Similarity 99.8%; Pred. No. 1.5e-170;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 NDVARGIVKADVAGSSGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db      207 NDVARGIVKADVAGSSGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 266

Qy      61 NANDTNGHGTIVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQSQAYS 120
Db      267 NANDTNGHGTIVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQSQAYS 326

Qy      121 AGARIHTNSWGAANGAVTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db      327 AGARIHTNSWGAANGAVTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386

Qy      181 TVGATENLRPFGSVADNINHVAQFSSRGPTKGRIKPDVMAPGTFILSARSSSLAPDSSF 240
Db      387 TVGATENLRPFGSVADNINHVAQFSSRGPTKGRIKPDVMAPGTFILSARSSSLAPDSSF 446

Qy      241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
Db      447 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 506

Qy      301 PNGNQGWRVTLDKSLNAVYVNESSSLSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db      507 PNGNQGWRVTLDKSLNAVYVNESSSLSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 566

Qy      361 SVTLVNDLDELVTAPNGTQYVGNDFTSYNDNWDGRNNVNFVINAPOSQYTTIEVOAYN 420
Db      567 SVTLVNDLDELVTAPNGTQYVGNDFTSYNDNWDGRNNVNFVINAPOSQYTTIEVOAYN 626

Qy      421 VPVGFQTFSLAIVN 434
Db      627 VPVGFQTFSLAIVN 640
```

Search completed: April 7, 2006, 09:42:50
Job time : 83 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: April 7, 2006, 09:42:58 ; Search time 83 Seconds
(without alignments)
163.100 Million cell updates/sec

Title: US-10-820-714A-1

Perfect score: 2247

Sequence: 1 NDVARGIVKADVAQSSVGLY.....EVQAINVPGQTFLAIVN 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 3119182 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_New:*
1: /SIDSS/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /SIDSS/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /SIDSS/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /SIDSS/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /SIDSS/ptodata/1/pubpaa/US05_NEW_PUB.pep:*
6: /SIDSS/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /SIDSS/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /SIDSS/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	286.5	12.8	802	6	US-10-510-386-2
2	253	11.3	874	6	US-10-510-386-28
3	253	11.3	1047	6	US-10-510-386-200
4	245	10.9	272	7	US-11-020-602-236
5	240	10.7	269	7	US-11-020-602-6
6	235.5	10.5	275	7	US-11-065-943-54
7	235.5	10.5	275	7	US-11-020-602-3
8	231.5	10.3	274	7	US-11-156-062-14
9	230.5	10.3	274	7	US-11-156-062-12
10	230.5	10.3	379	7	US-11-156-062-23
11	229.5	10.2	274	7	US-11-020-602-5
12	226.5	10.1	274	7	US-11-156-062-4
13	226.5	10.1	274	7	US-11-156-062-8
14	225.5	10.0	274	7	US-11-156-062-10
15	225.5	10.0	1052	7	US-11-020-602-208
16	224.5	10.0	274	7	US-11-156-062-6
17	223.5	9.9	275	7	US-11-020-602-4
18	221.5	9.9	274	7	US-11-156-062-16
19	221.5	9.9	274	7	US-11-156-062-18
20	220.5	9.8	274	7	US-11-156-062-2
21	219.5	9.8	382	7	US-11-020-602-2
22	209.5	9.3	280	7	US-11-020-602-209
23	205	9.1	1432	6	US-10-510-386-218
24	203	9.0	1647	7	US-11-052-554A-260
25	181	8.1	740	7	US-11-096-568A-24714

26	181	8.1	777	7	US-11-096-568A-24713	Sequence 24713, A
27	181	8.1	790	7	US-11-096-568A-24712	Sequence 24712, A
28	177	7.9	591	6	US-10-510-386-22	Sequence 22, Appl
29	167	7.4	722	7	US-11-096-568A-31863	Sequence 31863, A
30	167	7.4	757	7	US-11-096-568A-31862	Sequence 31862, A
31	167	7.4	798	7	US-11-096-568A-31861	Sequence 31861, A
32	167	7.1	659	7	US-11-096-568A-17896	Sequence 17896, A
33	160	7.1	671	7	US-11-096-568A-17895	Sequence 17895, A
34	160	7.1	791	7	US-11-096-568A-17894	Sequence 17894, A
35	158.5	7.1	733	7	US-11-096-568A-24028	Sequence 24028, A
36	158.5	7.1	759	7	US-11-096-568A-24027	Sequence 24027, A
37	158.5	7.1	764	7	US-11-096-568A-24026	Sequence 24026, A
38	156	6.9	791	7	US-11-096-568A-31251	Sequence 31251, A
39	155	6.9	672	7	US-11-096-568A-23983	Sequence 23983, A
40	155	6.9	680	7	US-11-096-568A-23982	Sequence 23982, A
41	152.5	6.8	794	7	US-11-218-986-2	Sequence 2, Appl
42	152.5	6.8	820	6	US-10-821-234-1176	Sequence 1176, Ap
43	144.5	6.4	617	7	US-11-096-568A-31252	Sequence 31252, A
44	136.5	6.1	3132	7	US-11-087-099-1245	Sequence 1245, Ap
45	136	6.1	418	7	US-11-096-568A-23984	Sequence 23984, A

ALIGNMENTS

RESULT 1
US-10-510-386-2
; Sequence 2, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-2

Query Match	12.8%	Score 286.5;	DB 6;	Length 802;
Best Local Similarity	23.0%	Pred. No. 3.9e-13;	Indels 231;	Gaps 27;
Matches 143;	Conservative 69;	Mismatches 178;		
Qy	2	DVARGIVKADVAQSSVGLYGQGI	VAVADTGLDTRND-SSNHAFRGK--	ITALYALGR 58
Db	158	DKSAPFGADQAWKS-GYTGKIKV	AVDITGVYTHPLKKNFGYKGYDF	VDNDYDQEQ 216
Qy	59	TNNANDTNG---HGTAVAGSVLGN	STNKGMAPQANLVFQSIMDSGGGLG	LPSNLQTLF 115
Db	217	TPTGPPRGGATDHGTHVAGTTAANG	QI-KGVAPEATLLAYRVLGPGG--	SGTTENVIAGI 273
Qy	116	SOAYSAGARIHTNSGAAVNGA-YT	DSRNVDYVKRNDMTILFAAGNEGNG	TISARG 174
Db	274	EKAVADGAKVMNLSLNSLSPDYAT	SI--ALDWAMAEVGVAVTSGNSGPN	WTGSPG 331
Qy	175	TAKNAITGATE-----NLRPSFG	-----	----- 194
Db	332	TSRVAISVGASQOLPYNEYSVTLPS	YSKVMGYQBEKLEALNGQEVLEAGL	QADDF 391
Qy	195	-----YADNINH-----	-----	----- 201
Db	392	SGKDVKGKVAIQRGVIFPVDKAEAK	NAIGAIVYNNATGEIEANVMGMAVPT	VKLK 451
Qy	202	-----VAQFSRGTGD--GRIKPDW	APGFTILSA 230	-----

Db 452 BEGELVQOIKEGKHSVVFSEFKLDKLGELTASFSRSGFVMDTMMIKPDVSAPGVNIVST 511
QY 231 RSSLAPDSFWANHDSK-----YAYMGTSMATPIVAGNVAQLREHFVKNRGITP--KPSL 284
Db 512 IPT-----HDPKPYGSGKQGTSMASPHVAGTAAILKQ-----AKPDWTEQ 554
QY 285 LKAALIAGAADI-----GLGYPNGNGWGRVTLTDLKSLNAVYVNESS----- 326
Db 555 IKGVLMTAEKLTDENGKPLPHNTQGAGSIRIMEALKASSIVTPGSHSYGTFLKDKGKQT 614
QY 327 -----LSTSQA-----TYSFTATAGKPLKISLVSD---APASIT---ASVTLYNDL 368
Db 615 KQAFTEIENLSHRKAYQLEYSFKGTG-----ITVSGTERVVVPANQTGKAAAKVTNSA 669
QY 369 DLVITAPNGTVQVGNDFTSYNDNDWGRNVE---NVFINAP-----QSGT 411
Db 670 KTKAGTYEGTVIRE-----DGRKVAEIPLLILVKEPDYPRVTSVTVPEGAKQGA 719
QY 412 YTIEVOAYNVPGPQTFFSLAI 432
Db 720 YTIE--AY-LPGGAELAPLV 737

RESULT 2

US-10-510-386-28
Query Match 11.3%; Score 253; DB 6; Length 874;
Best Local Similarity 27.2%; Pred. No. 1.2e-10;
Matches 95; Conservative 51; Mismatches 129; Indels 74; Gaps 13;
GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510.386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 874
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-28

QY 25 IVAVADTGLDGRNDSMHAEAFRGKI---TALYALGRTNANDTNGHGHVAGSVLG--- 78
Db 447 VIAVVDVTGVDHTLADLS-----GSVKKDEGYNVYGRGTADAMDDNGHGHVSGIIAAQD 500
QY 79 NGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYSAGARIHTNSWGAAVNGAY 138
Db 501 NHFSMAGINAYAKILPVKVLDSG--SGDTEQIANGIIYAADHGAKVINLSLG---GPY 554
QY 139 TTDSRNVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAITVGATENLRPSFGSYADN 198
Db 555 SRVMEYALKYAASKNVTTIVAATGNDGVS--EISYPASSKYTLSVGATNNL----- 602
QY 199 INHVAQFSSRGPTKDGRIKPDVMAPTGTFILSARSSLAPDSSFWANHDSKYAYMGTSMAT 258
Db 603 -DLVSDYSNYGKGL-----DMVAPGTDI-----PSLVPDGN-----VTYMSGTSMWA 643
QY 259 PIVAGNVAQLREHFVKNRGITPKPSLLKAAIAGAADIGL---GYPNGN----- 304
Db 644 PHVAAAAGLL-----LSQNPSLKPKQIASLLTETTADVAFEEQDNPNPDYDLIDIEPAAQI 698
QY 305 -----QWGRVTLDKSLNAVYVNESSLSLTSQKATYSFTATAGKPLKI 347
Db 699 PGYDFVSGWGRNLNVFHAASVFELNMKVHPVLNRHTAVTGTAKSGVTVKI 747

RESULT 3

US-10-510-386-200
Query Match 11.3%; Score 253; DB 6; Length 1047;
Best Local Similarity 27.2%; Pred. No. 1.5e-10;
Matches 95; Conservative 51; Mismatches 129; Indels 74; Gaps 13;
GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510.386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 200
; LENGTH: 1047
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-200

QY 25 IVAVADTGLDGRNDSMHAEAFRGKI---TALYALGRTNANDTNGHGHVAGSVLG--- 78
Db 447 VIAVVDVTGVDHTLADLS-----GSVKKDEGYNVYGRGTADAMDDNGHGHVSGIIAAQD 500
QY 79 NGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYSAGARIHTNSWGAAVNGAY 138
Db 501 NHFSMAGINAYAKILPVKVLDSG--SGDTEQIANGIIYAADHGAKVINLSLG---GPY 554
QY 139 TTDSRNVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAITVGATENLRPSFGSYADN 198
Db 555 SRVMEYALKYAASKNVTTIVAATGNDGVS--EISYPASSKYTLSVGATNNL----- 602
QY 199 INHVAQFSSRGPTKDGRIKPDVMAPTGTFILSARSSLAPDSSFWANHDSKYAYMGTSMAT 258
Db 603 -DLVSDYSNYGKGL-----DMVAPGTDI-----PSLVPDGN-----VTYMSGTSMWA 643
QY 259 PIVAGNVAQLREHFVKNRGITPKPSLLKAAIAGAADIGL---GYPNGN----- 304
Db 644 PHVAAAAGLL-----LSQNPSLKPKQIASLLTETTADVAFEEQDNPNPDYDLIDIEPAAQI 698
QY 305 -----QWGRVTLDKSLNAVYVNESSLSLTSQKATYSFTATAGKPLKI 347
Db 699 PGYDFVSGWGRNLNVFHAASVFELNMKVHPVLNRHTAVTGTAKSGVTVKI 747

RESULT 4

US-11-020-602-236
Query Match 11.3%; Score 253; DB 6; Length 874;
Best Local Similarity 27.2%; Pred. No. 1.2e-10;
Matches 95; Conservative 51; Mismatches 129; Indels 74; Gaps 13;
GENERAL INFORMATION:
; APPLICANT: Estell, David
; APPLICANT: Harding, Fiona
; TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND
; TITLE OF INVENTION: METHODS OF MAKING AND USING THE SAME
; FILE REFERENCE: GC527C2
; CURRENT APPLICATION NUMBER: US/11/020.602
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 09/500,135
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: US 09/060,872
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 236
; LENGTH: 272
; TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Hybrid of
OTHER INFORMATION: Bacillus lentus and Bacillus amyloliquefaciens
US-11-020-602-236

Query Match 10.9%; Score 245; DB 7; Length 272;
Best Local Similarity 32.7%; Pred. No. 1e-10;
Matches 86; Conservative 33; Mismatches 96; Indels 48; Gaps 11;

QY 8 VKADVAQSSYGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTRNNANDTNG 67
DB 11 VOAPAAHNR-GLTSGVKVAVLDTGIST-----HPDLNIRGGASFVPGEP-STQDNG 61
QY 68 HGTHVAGSV--LNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQSAYSAGARI 125
DB 62 HGTHVAGTIAALNNSIGVLGVAAPSALYAVKVLGASG--SGSVSSIAQGLEWAGNNGMHV 119
QY 126 HTNSGAAVNGAYTTDSRVDYVRKNDMTILFAAGNEGPNG--CTISAPGTAKNAITVG 183
DB 120 INMSLGGSGSAL-----KAAVDKAVASGVVVVAAAAGNEGTSGSSTVGYPGKYPVIAVG 175
QY 184 ATENLRPSFGSYADNINHVAFSSRGPTKDGRIKPDVMAPGTIFLSARSSLAPDSSFWAN 243
DB 176 A-----VDSNQRAFSFSSVGP-----ELDVMAPG---VSIQSTLP----- 207
QY 244 HDSKYAYMGTSMATPIVAGNVA 266
DB 208 -GNKYGAYNGTSMASPHVAGAAA 229

RESULT 5

US-11-020-602-6
Sequence 6, Application US/11020602
Publication No. US20060024764A1
GENERAL INFORMATION:
APPLICANT: Estell, David
APPLICANT: Harding, Fiona
TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND
TITLE OF INVENTION: METHODS OF MAKING AND USING THE SAME
FILE REFERENCE: GC527C2
CURRENT APPLICATION NUMBER: US/11/020,602
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: US 09/500,135
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: US 09/060,872
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 269
TYPE: PRT
ORGANISM: Bacillus lentus
US-11-020-602-6

Query Match 10.7%; Score 240; DB 7; Length 269;
Best Local Similarity 31.1%; Pred. No. 2.3e-10;
Matches 91; Conservative 30; Mismatches 90; Indels 82; Gaps 14;

QY 8 VKADVAQSSYGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTRNNANDTNG 67
DB 11 VOAPAAHNR-GLTSGVKVAVLDTGIST-----HPDLNIRGGASFVPGEP-STQDNG 61
QY 68 HGTHVAGSV--LNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQSAYSAGARI 125
DB 62 HGTHVAGTIAALNNSIGVLGVAAPSALYAVKVLGASG--SGSVSSIAQGLEWAGNNGMHV 119
QY 126 HTNSWGA-----AVNGAYTTDSRVDYVRKNDMTILFAAGNEGPNGGTISAPGTA 176
DB 120 ANLSLGSPPSATLEQAVNSA---TSRGV-----LVVAASGNSG--AGSISYPARY 165
QY 177 KNAITVGATE--NLRPSFGSYADNINHVAFSSRGPTKDGRIKPDVMAPGTIFLSARSSL 234

DB 166 ANAMAVGATDQNNNRASFSQYAGL-----DIVAPGVNVQSTYPG- 205
QY 235 APDSSFWANHDSKYAYMGTSMATPIVAGNVA-----QLRHFVKV 275
DB 206 -----STYASLNGTSMATPHVAGAAALVKQKNPSWSNVQIRNH-LKN 246

RESULT 6

US-11-065-943-54
Sequence 54, Application US/11065943
Publication No. US20050250131A1
GENERAL INFORMATION:
APPLICANT: JESTIN, JEAN-LUC
APPLICANT: VICHIER-GUERRE, SOPHIE
APPLICANT: FERRIS, STEPHANE
TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
FILE REFERENCE: 26642GUSDXCIP
CURRENT APPLICATION NUMBER: US/11/065,943
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: US 10/787,219
PRIOR FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 106
SOFTWARE: PatentIn version 3.3
SEQ ID NO 54
LENGTH: 275
TYPE: PRT
ORGANISM: Bacillus amyloliquefaciens
US-11-065-943-54

Query Match 10.5%; Score 235.5; DB 7; Length 275;

Best Local Similarity 30.9%; Pred. No. 5e-10; Indels 83; Gaps 12;
Matches 87; Conservative 27; Mismatches 85;

QY 8 VKADVAQSSYGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTRNNANDTNG 67
DB 11 IKAP-ALHSQGYTGSNVKVAVIDSGID-----SSHPDLKVAGGASWVPSEINPQDNNS 63
QY 68 HGTHVAGSV--LNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFQSAYSAGARI 125
DB 64 HGTHVAGTVAALNNSIGVLGVAAPSASLYAVKVLGADG-----SQGY----- 104
QY 126 HTNSGAAVNGAYTTDSRVD-----DYVRKNDMTILFAAGNEGP 166
DB 105 ---SW--IINGIEWAIANNMDVINMSLGGPSGAALKAAVDKAVASGVVVVAAAAGNEGTS 159
QY 167 G--GTISAPGTAKNAITVGATENLRPSFGSYADNINHVAFSSRGPTKDGRIKPDVMAPG 224
DB 160 GSSSTVGYPGKYPVIAVGA-----VDSNQRAFSFSSVGP-----ELDVMAPG 202
QY 225 TFIARSSSLAPDSSFWANHDSKYAYMGTSMATPIVAGNVA 266
DB 203 ---VSIQSTLP-----GNKYGAYNGTSMASPHVAGAAA 232

RESULT 7

US-11-020-602-3
Sequence 3, Application US/11020602
Publication No. US20060024764A1
GENERAL INFORMATION:
APPLICANT: Estell, David
APPLICANT: Harding, Fiona
TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND
TITLE OF INVENTION: METHODS OF MAKING AND USING THE SAME
FILE REFERENCE: GC527C2
CURRENT APPLICATION NUMBER: US/11/020,602
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: US 09/500,135
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: US 09/060,872
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 240

APPLICANT: Stehr, Regina
APPLICANT: Maurer, Karl-Heinz
TITLE OF INVENTION: SUBSTITUTED VARIANTS, WITH IMPROVED PERHYDROLASE ACTIVITY
FILE REFERENCE: HENK-0134 / H5698
CURRENT APPLICATION NUMBER: US/11/156,062
CURRENT FILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: PCT/EP2003/014127
PRIOR FILING DATE: 2003-12-20
PRIOR APPLICATION NUMBER: DE 102 60 903.9
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.3
SEQ ID NO 23
LENGTH: 379
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-11-156-062-23

Query Match 10.3%; Score 230.5; DB 7; Length 379;
Best Local Similarity 30.2%; Pred. No. 1.7e-09;
Matches 85; Conservative 37; Mismatches 106; Indels 53; Gaps 11;
QY 7 IVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTNNDTN 66
DB 115 LIKADKVQAQ-GFKGANVAVLDGTGIAQSHPLDNLVVG-----ASFVAGEAYN-TDGN 166
QY 67 GHGTHVAGSV--LNGSTNKGMAPOANLVFOSIMDSGGGLGSLPSNLQTLFSQAYSAGAR 124
DB 167 GHGTHVAGTVAALDNTTGVGVAPSVSLYAVKVLNLSG--SGSYSGIVSGIEWATTNGMD 224
QY 125 IHTNSGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPN--GTISAPGTAKNAITV 182
DB 225 VINMSLGA---SGSTAMKQAVDNAYARGVVVAAAGNSGSGNTNTTIGYPAKYDSVI 281
QY 183 GATENLRPSFGSYADNINHVAQPSRGPTKDGRIKPDVMAFGTFLSARSSSLAPDSSFWA 242
DB 282 GA-----VDSNSNRASFSSVG-----AELEVMAPGAGVYSTYPT----- 315
QY 243 NHDSKYAVMGTSMTATPIVAGNVA-----QLREHFVKNR 276
DB 316 ---NTYATLNGTSMASPHVAGAAALILSKHPNLSASQVRNR 353

RESULT 11
US-11-020-602-5
Sequence 5, Application US/11020602
Publication No. US20060024764A1
GENERAL INFORMATION:
APPLICANT: Estell, David
APPLICANT: Harding, Fiona
TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND
METHODS OF MAKING AND USING THE SAME
FILE REFERENCE: GC597C2
CURRENT APPLICATION NUMBER: US/11/020,602
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: US 09/500,135
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: US 09/060,872
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 274
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-11-020-602-5

Query Match 10.2%; Score 229.5; DB 7; Length 274;
Best Local Similarity 30.2%; Pred. No. 1.4e-09;
Matches 85; Conservative 37; Mismatches 106; Indels 53; Gaps 11;
QY 7 IVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTNNDTN 66

DB 10 LIKADKVQAQ-GFKGANVAVLDGTGIAQSHPLDNLVVG-----ASFVAGEAYN-TDGN 61
QY 67 GHGTHVAGSV--LNGSTNKGMAPOANLVFOSIMDSGGGLGSLPSNLQTLFSQAYSAGAR 124
DB 62 GHGTHVAGTVAALDNTTGVGVAPSVSLYAVKVLNLSG--SGSYSGIVSGIEWATTNGMD 119
QY 125 IHTNSGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPN--GTISAPGTAKNAITV 182
DB 120 VINMSLGA---SGSTAMKQAVDNAYARGVVVAAAGNSGSGNTNTTIGYPAKYDSVI 176
QY 183 GATENLRPSFGSYADNINHVAQPSRGPTKDGRIKPDVMAFGTFLSARSSSLAPDSSFWA 242
DB 177 GA-----VDSNSNRASFSSVG-----AELEVMAPGAGVYSTYPT----- 210
QY 243 NHDSKYAVMGTSMTATPIVAGNVA-----QLREHFVKNR 276
DB 211 ---NTYATLNGTSMASPHVAGAAALILSKHPNLSASQVRNR 248

RESULT 12
US-11-156-062-4
Sequence 4, Application US/11156062
Publication No. US20050281773A1
GENERAL INFORMATION:
APPLICANT: Wieland, Susanne
APPLICANT: Polanyi-Bald, Laura
APPLICANT: Prueser, Inken
APPLICANT: Stehr, Regina
TITLE OF INVENTION: SUBSTITUTED VARIANTS, WITH IMPROVED PERHYDROLASE ACTIVITY
FILE REFERENCE: HENK-0134 / H5698
CURRENT APPLICATION NUMBER: US/11/156,062
CURRENT FILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: PCT/EP2003/014127
PRIOR FILING DATE: 2003-12-20
PRIOR APPLICATION NUMBER: DE 102 60 903.9
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.3
SEQ ID NO 4
LENGTH: 274
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-11-156-062-4

Query Match 10.1%; Score 226.5; DB 7; Length 274;
Best Local Similarity 30.2%; Pred. No. 2.3e-09;
Matches 85; Conservative 36; Mismatches 107; Indels 53; Gaps 11;
QY 7 IVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTNNDTN 66
DB 10 LIKADKVQAQ-GFKGANVAVLDGTGIAQSHPLDNLVVG-----ASFVAGEAYN-TDGN 61
QY 67 GHGTHVAGSV--LNGSTNKGMAPOANLVFOSIMDSGGGLGSLPSNLQTLFSQAYSAGAR 124
DB 62 GHGTHVAGTVAALDNTTGVGVAPSVSLYAVKVLNLSG--SGSYSGIVSGIEWATTNGMD 119
QY 125 IHTNSGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPN--GTISAPGTAKNAITV 182
DB 120 VINMSLGA---SGSTAMKQAVDNAYARGVVVAAAGNSGSGNTNTTIGYPAKYDSVI 176
QY 183 GATENLRPSFGSYADNINHVAQPSRGPTKDGRIKPDVMAFGTFLSARSSSLAPDSSFWA 242
DB 177 GA-----VDSNSNRASFSSVG-----AELEVMAPGAGVYSTYPT----- 210
QY 243 NHDSKYAVMGTSMTATPIVAGNVA-----QLREHFVKNR 276
DB 211 ---NTYATLNGTSMASPHVAGAAALILSKHPNLSASQVRNR 248

RESULT 13

```
US-11-156-062-8
; Sequence 8, Application US/11156062
; Publication No. US20050281773A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Susanne
; APPLICANT: Polanyi-Bald, Laura
; APPLICANT: Prueser, Inken
; APPLICANT: Stehr, Regina
; APPLICANT: Maurer, Karl-Heinz
; TITLE OF INVENTION: SUBSTITUIN VARIANTS, WITH IMPROVED PERHYDROLASE ACTIVITY
; FILE REFERENCE: HENK-0134 / H5698
; CURRENT APPLICATION NUMBER: US/11/156,062
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: PCT/EP2003/014127
; PRIOR FILING DATE: 2003-12-20
; PRIOR APPLICATION NUMBER: DE 102 60 903.9
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-156-062-8

Query Match      10.1%; Score 226.5; DB 7; Length 274;
Best Local Similarity 29.5%; Pred. No. 2.3e-09;
Matches 85; Conservative 36; Mismatches 100; Indels 67; Gaps 12;

Qy 7 IVKADVAQSSYGLYGQGGQIVAVADTGLDTGRNDSMHEAFRGKITALYALGRTNANDTN 66
Db 10 LIKADKVAQ-GFGKANVAVLDGTGIQASHPDLNVVGG-----ASFVAGEAYNA-DGN 61

Qy 67 GHGTHVAGSV--LNGSTNKGMAPOANLVFQSIMDS--GGGLGGLPSNLQTLFSQ----- 117
Db 62 GHGTHVAGTVAALDNTTGVLGVAPEVSVLYAVKVLNLSGSGSVSGVSGIEWATTNDMDVI 121

Qy 118 AYSAGARHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGNG--GTISAPGT 175
Db 122 NMSLGGASGSTAMKQAVDNAYA-----RGVVVAAAGNSGSGGNTNTIGYPAK 169

Qy 176 AKNATTCATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSLA 235
Db 170 YDSVIAVGA-----VDSNSNRASFSSVG-----AELEVMAPGAGVYSTYPT-- 210

Qy 236 PDSSFANHDSKYAYMGGTSMATPIVAGNVA-----QLREHFVKNR 276
Db 211 -----NTYATWDGTSMAHPVAGAAALILSKHPNLSASQVRNR 248

RESULT 14
US-11-156-062-10
; Sequence 10, Application US/11156062
; Publication No. US20050281773A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Susanne
; APPLICANT: Polanyi-Bald, Laura
; APPLICANT: Prueser, Inken
; APPLICANT: Stehr, Regina
; APPLICANT: Maurer, Karl-Heinz
; TITLE OF INVENTION: SUBSTITUIN VARIANTS, WITH IMPROVED PERHYDROLASE ACTIVITY
; FILE REFERENCE: HENK-0134 / H5698
; CURRENT APPLICATION NUMBER: US/11/156,062
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: PCT/EP2003/014127
; PRIOR FILING DATE: 2003-12-20
; PRIOR APPLICATION NUMBER: DE 102 60 903.9
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
```

```
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-156-062-10

Query Match      10.0%; Score 225.5; DB 7; Length 274;
Best Local Similarity 30.2%; Pred. No. 2.7e-09;
Matches 85; Conservative 36; Mismatches 107; Indels 53; Gaps 11;

Qy 7 IVKADVAQSSYGLYGQGGQIVAVADTGLDTGRNDSMHEAFRGKITALYALGRTNANDTN 66
Db 10 LIKADKVAQ-GFGKANVAVLDGTGIQASHPDLNVVGG-----ASFVAGEAYNA-DGN 61

Qy 67 GHGTHVAGSV--LNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYSAGAR 124
Db 62 GHGTHVAGTVAALDNTTGVLGVAPEVSVLYAVKVLNLSG--SGSVSGVSGIEWATTNGMD 119

Qy 125 IHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGNG--GTISAPGTAKNAITV 182
Db 120 VINMSLGA---SGSTAMKQAVDNAYARGVVVVAAGNSGSGGNTNTIGYPAKYDSVIAV 176

Qy 183 GATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSLAPDSSFMA 242
Db 177 GA-----VDSNSNRASFSSVG-----AELEVMAPGAGVYSTYPT----- 210

Qy 243 NHDSKYAYMGGTSMATPIVAGNVA-----QLREHFVKNR 276
Db 211 ---NTYATWDGTSMAHPVAGAAALILSKHPNLSASQVRNR 248

RESULT 15
US-11-020-602-208
; Sequence 208, Application US/11020602
; Publication No. US20060024764A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David
; APPLICANT: Harding, Fiona
; TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND
; FILE REFERENCE: GC527C2
; CURRENT APPLICATION NUMBER: US/11/020,602
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 09/500,135
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: US 09/060,872
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 208
; LENGTH: 1052
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-020-602-208

Query Match      10.0%; Score 225.5; DB 7; Length 1052;
Best Local Similarity 26.7%; Pred. No. 1.5e-08;
Matches 117; Conservative 66; Mismatches 157; Indels 99; Gaps 26;

Qy 8 VKADVAQSSYGLYGQGGQIVAVADTGLDTGRNDSMHEAFRGKITALYALGRTNAN----- 63
Db 197 LQADVLM-QMGYTCANVRVAVFDTGL-----SEKHPFKN-----VKRTNNTNERTL 243

Qy 64 -DTNGHGTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 121
Db 244 DDGLGHGTFVAG-VIASMRECOGFPDAELHIFRVFTNN-----QVSYTSWFLDAFNY 295

Qy 122 GARHTNSWGAANGAYTTDSRNVDY--VRKNDMTILFAAGNEGNGGTTISAPCTAKNA 179
Db 296 AILKKIDVLNLSIGGPDFMDHPFVDKMWELTANNVIMVSAIGNDGPGLYGLTUNNPADQMDV 355

Qy 180 ITVGATENLRPSFGSYADNINHVAQFSSRG-----PTKDGRIKPDVMAPGTFILSARSS 233
```

Db	356	IGVGGID-----PEDNI---ARFSSRGMTTWELPGGYGRMKPDIV---TYGAGVRS	401
Qy	234	LAPDSFWANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKRGITPKPSLLKAALIAGA	293
Db	402	GVKGGC-----RALSGTSVASPVVAGAVTLLVSTVQKRELV--NPASMKQALIASA	450
Qy	294	ADIGLGPNGN--QGWGRVTLDKSLNV--AYVNESSLSLTS-----QKATYSFTATAGKP	344
Db	451	RRJ-----PGVNMFEQGHGKDLLRAYQILNSY--KQASLSPSYIDLTECPYMW-PYCSQP	504
Qy	345	LKISLWSDAPASTTASVTLVNDLDEL---VITAPNGTQYVGNDFTSFYNDNMDGRNNVEN	401
Db	505	-----IYGGCMP--TVVNVTLNGMGVGTGRIVDKPDWQPYL-----PQNG-----DNIEV	547
Qy	402	VF-----INAPQSGTYTIEV	416
Db	548	AFSYSSVLWFWGGLAISI	566

Search completed: April 7, 2006, 09:44:54
Job time : 84 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 7, 2006, 09:27:45 ; Search time 93 seconds
(without alignment)
2050.434 Million cell updates/sec

Title: US-10-820-714A-1-HIS15

Perfect score: 2251

Sequence: 1 NDVARGIVKADVAQHSYGLY.....EVQAYNPVGPQTFSIAVN 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A: Geneseq 21.*
- 1: Geneseqp1980s.*
 - 2: Geneseqp1990s.*
 - 3: Geneseqp2000s.*
 - 4: Geneseqp2001s.*
 - 5: Geneseqp2002s.*
 - 6: Geneseqp2003as.*
 - 7: Geneseqp2003bs.*
 - 8: Geneseqp2004s.*
 - 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2248	99.9	434	8	ADs14438
2	2247	99.8	434	8	ADs14439
3	2242	99.6	434	5	AAm50080
4	2242	99.6	434	7	ADY33778
5	2242	99.6	434	7	ADs1757
6	2242	99.6	434	8	ADL25802
7	2242	99.6	434	8	ADm40771
8	2242	99.6	434	8	ADs14427
9	2242	99.6	434	8	ADT49604
10	2242	99.6	640	2	AAy17090
11	2242	99.6	640	8	ADm40773
12	2242	99.6	640	8	ADs14437
13	2242	99.6	641	8	ADT49613
14	2239	99.5	434	8	ADs14443
15	2237	99.4	434	8	ADm40780
16	2237	99.4	434	8	ADs14441
17	2237	99.4	640	2	AAy17091
18	2234	99.2	434	8	ADs14444
19	2234	99.2	434	8	ADs14442
20	2227	98.9	434	8	ADs14440
21	2219	98.6	434	8	ADs14445
22	2190	97.3	436	8	ADm40787
23	2186	97.1	434	5	AAm50081
24	2186	97.1	434	7	ADs251758

25	2186	97.1	434	8	ADm40779
26	2178	96.8	639	2	AAy17089
27	2150	95.5	639	2	AAy17087
28	2150	95.5	640	2	AAy17088
29	2138	95.0	434	5	AAm50085
30	2138	95.0	434	7	ADs251762
31	2138	95.0	434	8	ADm40784
32	2130.5	94.6	433	8	ADs2078
33	2130.5	94.6	433	8	ADs2011
34	2129.5	94.6	433	8	ADs2082
35	2126.5	94.5	433	8	ADs2083
36	2125.5	94.4	433	5	AAm50086
37	2125.5	94.4	433	7	ADs251763
38	2125.5	94.4	433	8	ADm40785
39	2125.5	94.4	433	8	ADs2010
40	2125.5	94.4	433	8	ADs2016
41	2125.5	94.4	433	8	ADs2001
42	2125.5	94.4	641	2	AAW89547
43	2123.5	94.3	433	8	ADs2062
44	2123.5	94.3	433	8	ADs2054
45	2122.5	94.3	433	8	ADs2087

ALIGNMENTS

RESULT 1
ADs14438
ID ADs14438 standard; protein; 434 AA.
XX
AC ADs14438;
XX
DT 30-DEC-2004 (first entry)
XX
DE Bacillus alkaline protease KP43 S15H/S16T mutant.
XX
KW protease; enzyme; alkaline protease; laundry detergent; KP43; mutant;
KW mutain.
XX
OS Bacillus sp.; KSM-KP43.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 15 /note= "Wild-type Ser substituted by His"
FT Misc-difference 16 /note= "Wild-type Ser substituted by Thr"
XX
PN EP1466962-Al.

XX
PD 13-OCT-2004.
XX
PF 08-APR-2004; 2004EP-00008604.
XX
PR 10-APR-2003; 2003JP-00106709.
XX
PA (KAOS) KAO CORP.
XX
PI Okuda M, Sato T, Takimura Y, Sumitomo N, Kobayashi T;
XX
DR WPI; 2004-711313/70.
XX
PT New engineered alkaline protease, useful particularly in laundry
XX
PT detergents, comprising specified amino acids at particular positions.
XX
PS Example 1; Page; 31pp; English.
XX
CC The invention relates to a novel alkaline protease. The new alkaline
XX
CC protease comprises an amino acid sequence in which one or more amino acid
XX
CC residues selected from those located at 7 specific positions within
XX
CC ADs14427, or at positions corresponding to these positions are: position
XX
CC 15 (histidine), position 16 (threonine or glutamine), position 166
XX
CC (glycine), position 167 (valine), position 197 (serine), position 346

CC (arginine), and position 405 (aspartic acid). The alkaline protease is
CC useful in industry particularly in laundry detergents, but also e.g. in
CC fibre modifying agents, leather processing agents, cosmetic compositions,
CC bath additives, food-modifying agents, and pharmaceuticals. The present
CC sequence represents an alkaline protease variant of the invention. Note:
CC The present sequence is not represented in the specification, but has
CC been created by the indexer using sequence shown in ADS14427 and
CC information given in Example 1.
XX
XX
SQ Sequence 434 AA;

Query Match 99.9%; Score 2248; DB 8; Length 434;
Best Local Similarity 99.8%; Pred. No. 5.4e-160;
Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
QY 61 NANTNGHGTTHVAGSVLGNSTNKGMAPOANLVFOSIMDSGGGLGSLPSNLQTLFSQAYS 120
Db 61 NANTNGHGTTHVAGSVLGNSTNKGMAPOANLVFOSIMDSGGGLGSLPSNLQTLFSQAYS 120
QY 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPYKDGRIKPDVMAPGTIFILSARSLAPDSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSRGPYKDGRIKPDVMAPGTIFILSARSLAPDSF 240
QY 241 WANHDSKYAYMGTSNATPIVAGNVAQLREHFVKRGTTPKPSLLKAALIAAGADIGLY 300
Db 241 WANHDSKYAYMGTSNATPIVAGNVAQLREHFVKRGTTPKPSLLKAALIAAGADIGLY 300
QY 301 PNGNGQWGRVTLDKSLNVAAYNNESSLSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 301 PNGNGQWGRVTLDKSLNVAAYNNESSLSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWNGRNNVNFVINAPOSQGTITIEVQAYN 420
Db 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWNGRNNVNFVINAPOSQGTITIEVQAYN 420
QY 421 VPVGPQTFLAIVN 434
Db 421 VPVGPQTFLAIVN 434

RESULT 2
ADS14439
ID ADS14439 standard; protein; 434 AA.
XX
AC ADS14439;
XX AC
DT 30-DEC-2004 (first entry)
XX
DE Bacillus alkaline protease KP43 S15H/S16Q mutant.
XX
KW protease; enzyme; alkaline protease; laundry detergent; KP43; mutant;
KW mutain.
XX
OS Bacillus sp.; KSM-KP43.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 15
FT /note= "Wild-type Ser substituted by His"
FT Misc-difference 16
FT /note= "Wild-type Ser substituted by Gln"
XX
PN EP1466962-A1.
XX
PD 13-OCT-2004.

XX 08-APR-2004; 2004EP-00008604.
XX
XX
PR 10-APR-2003; 2003JP-00106709.
XX
XX (KAOS) KAO CORP.
XX
XX Okuda M, Sato T, Takimura Y, Sumitomo N, Kobayashi T;
XX
XX WPI; 2004-711313/70.
XX
XX New engineered alkaline protease, useful particularly in laundry
PT detergents, comprising specified amino acids at particular positions.
PT
XX
XX Example 1; Page; 31pp; English.
XX
XX The invention relates to a novel alkaline protease. The new alkaline
CC protease comprises an amino acid sequence in which one or more amino acid
CC residues selected from those located at 7 specific positions within
CC ADS14427, or at positions corresponding to these positions are: position
CC 15 (histidine), position 16 (threonine or glutamine), position 166
CC (glycine), position 167 (valine), position 187 (serine), position 346
CC (arginine), and position 405 (aspartic acid). The alkaline protease is
CC useful in industry particularly in laundry detergents, but also e.g. in
CC fibre modifying agents, leather processing agents, cosmetic compositions,
CC bath additives, food-modifying agents, and pharmaceuticals. The present
CC sequence represents an alkaline protease variant of the invention. Note:
CC The present sequence is not represented in the specification, but has
CC been created by the indexer using sequence shown in ADS14427 and
CC information given in Example 1.
XX
XX
SQ Sequence 434 AA;

Query Match 99.8%; Score 2247; DB 8; Length 434;
Best Local Similarity 99.8%; Pred. No. 6.5e-160;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
QY 61 NANTNGHGTTHVAGSVLGNSTNKGMAPOANLVFOSIMDSGGGLGSLPSNLQTLFSQAYS 120
Db 61 NANTNGHGTTHVAGSVLGNSTNKGMAPOANLVFOSIMDSGGGLGSLPSNLQTLFSQAYS 120
QY 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPYKDGRIKPDVMAPGTIFILSARSLAPDSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSRGPYKDGRIKPDVMAPGTIFILSARSLAPDSF 240
QY 241 WANHDSKYAYMGTSNATPIVAGNVAQLREHFVKRGTTPKPSLLKAALIAAGADIGLY 300
Db 241 WANHDSKYAYMGTSNATPIVAGNVAQLREHFVKRGTTPKPSLLKAALIAAGADIGLY 300
QY 301 PNGNGQWGRVTLDKSLNVAAYNNESSLSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 301 PNGNGQWGRVTLDKSLNVAAYNNESSLSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWNGRNNVNFVINAPOSQGTITIEVQAYN 420
Db 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWNGRNNVNFVINAPOSQGTITIEVQAYN 420
QY 421 VPVGPQTFLAIVN 434
Db 421 VPVGPQTFLAIVN 434
RESULT 3
AAM50080
ID AAM50080 standard; protein; 434 AA.

AC AAM50080;
XX
XX
DT 12-AUG-2002 (first entry)
XX
DE Bacillus sp KSM-KP43 alkaline protease protein fragment.
XX
XX Alkaline protease; detergent; laundry; bleaching; dishwasher.
XX
OS Bacillus sp.
XX
PN EP1209233-A2.
XX
XX 29-MAY-2002.
XX
XX 22-NOV-2001; 2001EP-00127851.
XX
XX 22-NOV-2000; 2000JP-00355166.
PR
PR 12-APR-2001; 2001JP-00114048.
XX
XX (KAOS) KAO CORP.
XX
XX Hatada Y, Ogawa A, Kageyama Y, Sato T, Araki H, Sumitomo N;
PI Okuda M, Saeki K;
XX
XX WPI; 2002-437518/47.
DR
XX
XX New modified alkaline proteases useful in detergent compositions.
XX
XX Claim 1; Page 10-11; 25pp; English.
XX
XX This invention describes novel Bacillus sp. alkaline proteases useful in
CC detergent compositions, especially in laundry, bleaching or automatic
CC dishwasher detergents. The novel proteases have an increased detergency %
CC (34 - 38%) compared to prior art alkaline proteases (31 and 23%). This
CC sequence represents a fragment of the alkaline protease KP43 from
CC Bacillus sp strain KSM-KP43 which is used to create the modified protease
CC represented in AAM50090
XX
SQ Sequence 434 AA;
Query Match 99.6%; Score 2242; DB 5; Length 434;
Best Local Similarity 99.8%; Pred. No. 1.5e-159;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDGRNDSMHEAFRGKITALYALGRTN 60
DB 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGRNDSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNGHGTAVGSLVNGSTNKGMAPOANLVFQSIQSDSGGLGLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGTAVGSLVNGSTNKGMAPOANLVFQSIQSDSGGLGLPSNLQTLFSQAYS 120
QY 121 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNCGTISAPGTAKNAI 180
DB 121 AGARIHTNSGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNCGTISAPGTAKNAI 180
QY 181 TVGATENLRPFSFGSYADNHNHVAQFSRGTGDKRIKPDVMAFGTIFLSARSLAPDSF 240
DB 181 TVGATENLRPFSFGSYADNHNHVAQFSRGTGDKRIKPDVMAFGTIFLSARSLAPDSF 240
QY 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADTGLGY 300
DB 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAAGADTGLGY 300
QY 301 PNGNQGWGVTLDKSLNVAYNVNESSLSQKATYSFTATAGKPLKISLVNSDAPASTTA 360
DB 301 PNGNQGWGVTLDKSLNVAYNVNESSLSQKATYSFTATAGKPLKISLVNSDAPASTTA 360
QY 361 SVTLVNDLVLVTAPNGTVGVNDFTSPYNDNWDGRNNVFNAPQSGTGTITIEVQAYN 420
DB 361 SVTLVNDLVLVTAPNGTVGVNDFTSPYNDNWDGRNNVFNAPQSGTGTITIEVQAYN 420

QY 421 VPVGPOTFSLAIWN 434
DB 421 VPVGPOTFSLAIWN 434
RESULT 4
ADY33778
ID ADY33778 standard; protein; 434 AA.
XX
XX ADY33778;
XX
XX 05-MAY-2005 (first entry)
XX
XX Bacillus species alkaline protease.
DE
XX
XX mutagenesis; alkaline protease; detergent; laundry; cosmetic; food;
KW bleaching detergent.
XX
XX Bacillus sp.
OS
XX EP1347044-A2.
PN
XX
XX 24-SEP-2003.
XX
XX 21-MAR-2003; 2003EP-00006472.
XX
XX 22-MAR-2002; 2002JP-00081428.
PR
PR 06-JUN-2002; 2002JP-00165987.
PR
PR 18-OCT-2002; 2002JP-00304230.
XX
XX 18-OCT-2002; 2002JP-00304231.
XX
XX (KAOS) KAO CORP.
PA
XX
XX Okuda M, Sato T, Saito K, Sumitomo N, Izawa Y, Saeki K;
PI Kobayashi T, Nomura M;
XX
XX WPI; 2003-846540/79.
DR N-PSDB; ADY33779.
XX
XX
PT New alkaline protease having specific amino acid residue at a specific
PT position of its amino acid sequence, useful for producing detergent
PT compositions, laundry detergent, fiber modifiers, leather-treating agents
PT or pipe cleaners.
XX
PS Claim 1; SEQ ID NO 1; 31pp; English.
XX
XX The invention relates to an alkaline protease having a fully defined
CC sequence of 434 amino acids (I) given in the specification, or an amino
CC acid sequence at least 80% homology with (I), where an amino acid residue
CC at position 65, 101, 163, 170, 171, 273, 320, 359 or 387 of (I) is
CC selected from 16 amino acid residues. The amino acid residues at the
CC corresponding positions are selected from: position 65: proline; position
CC 101: asparagine; position 163: histidine, aspartic acid, phenylalanine,
CC lysine, asparagine, serine, isoleucine, leucine, glutamine, threonine or
CC valine; position 170: valine or leucine; position 171: alanine, glutamic
CC acid, glycine or threonine; position 273: isoleucine, glycine or
CC threonine; position 320: phenylalanine, valine, threonine, leucine,
CC isoleucine or glycine; position 359: serine, leucine, valine, isoleucine
CC or glutamic acid; and position 387: alanine, lysine, glutamine, glutamic
CC acid, arginine or histidine. The alkaline protease is useful for the
CC production of a detergent composition, such as laundry detergent, fiber
CC modifiers, leather-treating agents, cosmetic compositions, bath
CC additives, food modifiers and pharmaceutical compositions. The alkaline
CC protease may also be used as bleaching detergent, hard surface cleaning
CC detergent, pipe cleaner, artificial tooth cleaner, and as a sterilizing
CC cleanser for medical tools. The new alkaline protease has a more potent
CC proteolytic capacity, exhibiting excellent detergency for the removal of
CC a complex stain, and has high secretion capacity. This sequence
XX corresponds to the Bacillus sp. alkaline protease.
SQ Sequence 434 AA;

Query Match 99.6%; Score 2242; DB 7; Length 434;

Best Local Similarity 99.8%; Pred. No. 1.5e-159;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60

QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120

QY 121 AGARITHNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 121 AGARITHNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180

QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPDKGRIKPDVMAPGTFILSARSSSLAPDSF 240
DB 181 TVGATENLRPSFGSYADNINHVAQFSRGPDKGRIKPDVMAPGTFILSARSSSLAPDSF 240

QY 241 WANHDSKYAYMGTSWATPIVAGNVAQLREHFVKNGRITPKPSLLKAALIAGAADIGLGY 300
DB 241 WANHDSKYAYMGTSWATPIVAGNVAQLREHFVKNGRITPKPSLLKAALIAGAADIGLGY 300

QY 301 PNGNQGWGRVTLDKSLNVAAYVNESSLSSTSKATYSFTATAGKPLKISLVMSDAPASTTA 360
DB 301 PNGNQGWGRVTLDKSLNVAAYVNESSLSSTSKATYSFTATAGKPLKISLVMSDAPASTTA 360

QY 361 SVTLVNDLDLVTAPNGTQYVGNDFTPSYNDNWDGRNNVNFVINAPOS GTTIEVQAYN 420
DB 361 SVTLVNDLDLVTAPNGTQYVGNDFTPSYNDNWDGRNNVNFVINAPOS GTTIEVQAYN 420

QY 421 VPVGPQTFSLAIVN 434
DB 421 VPVGPQTFSLAIVN 434

RESULT 5
ID ADZ51757 standard; protein; 434 AA.
XX ADZ51757;
AC ADZ51757;
XX 16-JUN-2005 (first entry)
DT Wild-type Bacillus sp. alkali protease.
XX alkali protease; enzyme; surfactant; mutagenesis.
XX Bacillus sp.
XX JP2003125783-A.
PN 07-MAY-2003.
PD 26-OCT-2001; 2001JP-00329472.
XX 26-OCT-2001; 2001JP-00329472.
PR (KAOS) KAO CORP.
XX WPI; 2003-856569/80.
DR New alkali protease useful for preparing detergents comprises
XX substitution mutations at 251 or 256 position of protease KP43 derived
PT from Bacillus species KSM-KP43.
XX Claim 1; SEQ ID NO 1; 16pp; Japanese.
PS The invention relates to a mutant alkali protease having an amino acid
XX deletion at position(s) 251 or 256 in a fully defined sequence given as
CC SEQ ID No:1 in the specification, or the following amino acid residue
CC Asp, Gly, Ala, Asp, Thr, Ile, Val, Leu or Glu at position 251, or the
XX amino acid residue Lys, Ser Phe, Arg, Tyr, Met, Thr, Ile, Val, Leu, or

CC Glu at position 256. Also described are: (i) an alkali protease having
CC the amino acid sequence of SEQ ID No:1, or having 60% or more homology to
CC SEQ ID No:1, or a deletion of amino acid corresponding to position 251 or
CC 256, (ii) a gene which encodes an alkali protease, (iii) a recombinant
CC vector containing the gene, and (iv) a transformed organism containing
CC the recombinant vector. The alkali protease sequence having 60% or more
CC homology to SEQ ID No:1 is chosen from a fully defined sequence selected
CC from SEQ ID Nos 2-7 as given in the specification. The transform
CC organism is a microorganism. The mutant alkali protease is useful for
CC preparing detergents. The mutant alkali protease exhibits high resistance
CC against oxidizing agent. The mutant alkali protease has high specific
CC activity. This sequence represents wild-type Bacillus sp. alkali
XX protease.
XX Sequence 434 AA;
QY Sequence 434 AA;
Query Match 99.6%; Score 2242; DB 7; Length 434;
Best Local Similarity 99.8%; Pred. No. 1.5e-159;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60

QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120

QY 121 AGARITHNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 121 AGARITHNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180

QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPDKGRIKPDVMAPGTFILSARSSSLAPDSF 240
DB 181 TVGATENLRPSFGSYADNINHVAQFSRGPDKGRIKPDVMAPGTFILSARSSSLAPDSF 240

QY 241 WANHDSKYAYMGTSWATPIVAGNVAQLREHFVKNGRITPKPSLLKAALIAGAADIGLGY 300
DB 241 WANHDSKYAYMGTSWATPIVAGNVAQLREHFVKNGRITPKPSLLKAALIAGAADIGLGY 300

QY 301 PNGNQGWGRVTLDKSLNVAAYVNESSLSSTSKATYSFTATAGKPLKISLVMSDAPASTTA 360
DB 301 PNGNQGWGRVTLDKSLNVAAYVNESSLSSTSKATYSFTATAGKPLKISLVMSDAPASTTA 360

QY 361 SVTLVNDLDLVTAPNGTQYVGNDFTPSYNDNWDGRNNVNFVINAPOS GTTIEVQAYN 420
DB 361 SVTLVNDLDLVTAPNGTQYVGNDFTPSYNDNWDGRNNVNFVINAPOS GTTIEVQAYN 420

QY 421 VPVGPQTFSLAIVN 434
DB 421 VPVGPQTFSLAIVN 434

RESULT 6
ADL25802
ID ADL25802 standard; protein; 434 AA.
XX ADL25802;
AC ADL25802;
XX 20-MAY-2004 (first entry)
DT Bacillus alkaline protease.
XX Bacillus alkaline protease.
DE alkaline protease; washing agent; enzyme.
XX Bacillus sp.
XX JP2004008085-A.
PN 15-JAN-2004.
PD 06-JUN-2002; 2002JP-00165950.
XX

```

PR 06-JUN-2002; 2002JP-00165950..
XX (KAOS ) KAO CORP.
XX
XX PA
XX
XX DR WPI; 2004-094297/10.
XX DR N-PSDB; ADL25803.
XX
XX PT Novel mutant alkaline protease produced by substituting the amino acid
XX residues useful as washing agent.
XX
XX PS Claim 1; SEQ ID NO 1; 21pp; Japanese.
XX
XX CC The invention comprises a mutant Bacillus alkaline protease which
XX contains substitutions at positions 163, 170 and 434. The mutant alkaline
XX protease is useful as a washing agent. The present amino acid sequence
XX represents a Bacillus alkaline protease of the invention.
XX
XX SQ Sequence 434 AA;

Query Match          99.6%; Score 2242; DB 8; Length 434;
Best Local Similarity 99.8%; Pred.No.1.5e-159;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
DB 121 AGARHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSYADNINHVAQFSRGTQDGRIPKDVMAAGTPILSARSLAPDSSF 240
DB 181 TVGATENLRPSFGSYADNINHVAQFSRGTQDGRIPKDVMAAGTPILSARSLAPDSSF 240
QY 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKRGIITPKPSLLKAALIAGAADIGLY 300
DB 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKRGIITPKPSLLKAALIAGAADIGLY 300
QY 301 PNGNQGWGRVTLDKSLNVAYNVNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360
DB 301 PNGNQGWGRVTLDKSLNVAYNVNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNDGRNNVENVFINAPQSGTYYTIEVOAYN 420
DB 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNDGRNNVENVFINAPQSGTYYTIEVOAYN 420
QY 421 VPVGPQTFFSLAIVN 434
DB 421 VPVGPQTFFSLAIVN 434

RESULT 7
ADM40771
ID ADM40771 standard; protein; 434 AA.
XX
XX AC ADM40771;
XX
XX DX 01-JUL-2004 (first entry)
XX
XX DE Mature alkaline protease from Bacillus sp. KSM-KP43.
XX
XX DE alkaline protease; laundry detergent; bleaching agent; detergent;
XX denture-cleaning agent; enzyme.
XX
XX OS Bacillus sp.; KSM-KP43.
XX
XX PN US2004072321-A1.
XX
```

ADS14427
ID ADS14427 standard; protein; 434 AA.
XX
AC ADS14427;
XX
XX
DT 30-DEC-2004 (first entry)
XX
DE Bacillus alkaline protease KP43 mature protein SEQ ID NO:1.
XX
XX
KW protease; enzyme; alkaline protease; laundry detergent; KP43.
XX
XX
OS Bacillus sp.; KSM-KP43.
XX
XX
PN EPI466962-A1.
XX
PD 13-OCT-2004.
XX
XX
PF 08-APR-2004; 2004EP-00008604.
XX
PR 10-APR-2003; 2003JP-00106709.
XX
PA (KAOS) KAO CORP.
XX
PI Okuda M, Sato T, Takimura Y, Sumitomo N, Kobayashi T;
XX
DR WPI; 2004-711313/70.
XX
DR N-PSDB; ADS14428.
XX
PT New engineered alkaline protease, useful particularly in laundry
PT detergents, comprising specified amino acids at particular positions.
XX
XX
PS Claim 1; SEQ ID NO 1; 31pp; English.
XX
XX
CC The invention relates to a novel alkaline protease. The new alkaline
CC protease comprises an amino acid sequence in which one or more amino acid
CC residues selected from those located at 7 specific positions within
CC ADS14427, or at positions corresponding to these positions are: position
CC 15 (histidine), position 16 (threonine or glutamine), position 166
CC (glycine), position 167 (valine), position 187 (serine), position 346
CC (arginine), and position 405 (aspartic acid). The alkaline protease is
CC useful in industry particularly in laundry detergents, but also e.g. in
CC fibre modifying agents, leather processing agents, cosmetic compositions,
CC bath additives, food-modifying agents, and pharmaceuticals. The present
CC sequence represents the wild-type Bacillus sp. KSM-KP43 alkaline
CC protease, KP43.
XX
SQ Sequence 434 AA;

Query Match 99.6%; Score 2242; DB 8; Length 434;
Best Local Similarity 99.8%; Pred. No. 1.5e-159;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDGRNDSMHEAFRGKITALYALGRTN 60
DB 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGRNDSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNGHGTGTVAGSVLGNSTNKGMAPOANLVFOSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGTGTVAGSVLGNSTNKGMAPOANLVFOSIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARIHTNSWGAANVGAYTTDSRNDDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
DB 121 AGARIHTNSWGAANVGAYTTDSRNDDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSGVSADNINHVAQSSRGPTKDGRIKPDVMAPGTIFILSARSLAPDSF 240
DB 181 TVGATENLRPSGVSADNINHVAQSSRGPTKDGRIKPDVMAPGTIFILSARSLAPDSF 240
QY 241 WANHDSKYAYMGTSWATPIVAGNVAQLREHFVKRGITPKPSLLKAALIAGAADIGLGY 300
DB 241 WANHDSKYAYMGTSWATPIVAGNVAQLREHFVKRGITPKPSLLKAALIAGAADIGLGY 300
QY 301 PNGNQGWGRVTLDKSLINVAYNNESSLSLTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360

DB 301 PNGNQGWGRVTLDKSLINVAYNNESSLSLTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
QY 361 SVTLVNDLDELVTAPNGTQYVGNDFTSFYNDNWDGRNNVENVFINAPQSQTIVIEVQAYN 420
DB 361 SVTLVNDLDELVTAPNGTQYVGNDFTSFYNDNWDGRNNVENVFINAPQSQTIVIEVQAYN 420
QY 421 VPVGPQTFSLAIVN 434
DB 421 VPVGPQTFSLAIVN 434
RESULT 9
ADT49604
ID ADT49604 standard; protein; 434 AA.
XX
AC ADT49604;
XX
DT 30-DEC-2004 (first entry)
XX
DE Bacillus alkaline protease mature protein fragment.
XX
KW Alkaline protease; detergent; fiber modification; leather processing;
KW cosmetic; bath additives; food-modification; pharmaceutical; enzyme.
XX
OS Bacillus sp. KSM-KP43.
XX
PN EPI466970-A1.
XX
PD 13-OCT-2004.
XX
PF 08-APR-2004; 2004EP-00008605.
XX
PR 10-APR-2003; 2003JP-00106708.
XX
PA (KAOS) KAO CORP.
XX
PI Sato T, Okuda M, Koyama S, Izawa Y, Kobayashi T;
XX
DR WPI; 2004-711313/70.
XX
DR N-PSDB; ADT49605.
XX
PT New engineered alkaline protease with improved activity and thermal
PT stability, useful particularly in detergents such as laundry detergents.
XX
XX
PS Claim 1; SEQ ID NO 1; 35pp; English.
XX
XX
CC The invention relates to an alkaline protease and its encoding gene. The
CC alkaline protease can be expressed by standard recombinant methodology.
CC The alkaline protease is useful in the industry particularly in
CC detergents such as laundry detergents, but also in fiber modifying
CC agents, leather processing agents, cosmetic compositions, bath additives,
CC food-modifying agents, and pharmaceuticals. The enzyme has good activity
CC and thermal stability. The present sequence represents a mature alkaline
XX protease from Bacillus sp. KSM-KP43.
SQ Sequence 434 AA;

Query Match 99.6%; Score 2242; DB 8; Length 434;
Best Local Similarity 99.8%; Pred. No. 1.5e-159;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDGRNDSMHEAFRGKITALYALGRTN 60
DB 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGRNDSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNGHGTGTVAGSVLGNSTNKGMAPOANLVFOSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGTGTVAGSVLGNSTNKGMAPOANLVFOSIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARIHTNSWGAANVGAYTTDSRNDDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
DB 121 AGARIHTNSWGAANVGAYTTDSRNDDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180

QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFLSARSLAPDSSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFLSARSLAPDSSF 240
QY 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNGRITPKPSLLKAALIAGAADIGLGY 300
Db 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNGRITPKPSLLKAALIAGAADIGLGY 300
QY 301 PNGNOGWGRVTLDKSLNVAIVNNESSLSSTQKATYSFTATAGKPLKISLWSDAPASTTA 360
Db 301 PNGNOGWGRVTLDKSLNVAIVNNESSLSSTQKATYSFTATAGKPLKISLWSDAPASTTA 360
QY 361 SVTLVNDLDELVTAPNGTQVGNDEFTSPYNDNWDGRNNVENFINAPQSGTYYTIEVOAYN 420
Db 361 SVTLVNDLDELVTAPNGTQVGNDEFTSPYNDNWDGRNNVENFINAPQSGTYYTIEVOAYN 420
QY 421 VPVGPQTFLSIAVN 434
Db 421 VPVGPQTFLSIAVN 434
RESULT 10
AAY17090
ID AAY17090 standard; protein; 640 AA.
XX AAY17090;
XX
DT 20-MAR-2003 (revised)
DT 21-JUL-1999 (first entry)
XX
DE Bacillus alkaline protease.
XX
KW Alkaline protease; Bacillus; casein digestion; oleic acid; enzyme;
KW washing composition; oxidising agent.
XX
OS Bacillus sp.
XX
PN WO9918218-Al.
XX
PD 15-APR-1999.
XX
PF 07-OCT-1998; 98WO-JP004528.
XX
PR 07-OCT-1997; 97JP-00274570.
XX
PA (KAOS) KAO CORP.
XX
PI Takaiwa M, Okuda M, Saeki K, Kubota H, Hitomi J, Kageyama Y;
PI Shikata S, Nomura M;
XX
DR WPI; 1999-287736/27.
DR N-PSDB; AAX37278.
XX
PT Alkali protease from Bacillus used in washing powders.
XX
PS Disclosure; Page 58-63; 71pp; Japanese.
XX
CC The invention relates to alkaline proteases produced by strains of
CC Bacillus. The proteases ability to digest casein is not inhibited by
CC oleic acid and they have a high stability to oxidising agents. The
CC alkaline protease of the invention has the following properties: (a) it
CC is active over the pH range 4-13 and has at least 80% of its optimum
CC activity over the pH range 6-12; (b) after 30 minutes at 40 deg. C it is
CC stable over the pH range 6-11; c) its isoelectric point is 8.9-9.1; (d)
CC its ability to digest casein is not inhibited by oleic acid; (e) it has
CC molecular weight about 43,000 by SDS-PAGE. The alkaline proteases can be
CC used as enzymes in washing compositions for use in automatic dishwashers
CC and for washing clothes. The stability to oxidising agents allows the
CC enzyme to be an effective component of washing compositions including
CC bleaches. The present sequence represents an alkaline protease. (Updated
CC on 20-MAR-2003 to correct DR field.)
XX

SQ Sequence 640 AA;

Query Match 99.6%; Score 2242; DB 2; Length 640;
Best Local Similarity 99.8%; Pred. No. 2.6e-159;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 207 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 266
QY 61 NANDTNGHGTHTVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGSLPSNLQTLFQAYS 120
Db 267 NANDTNGHGTHTVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGSLPSNLQTLFQAYS 326
QY 121 AGARHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 327 AGARHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFLSARSLAPDSSF 240
Db 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTFLSARSLAPDSSF 446
QY 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNGRITPKPSLLKAALIAGAADIGLGY 300
Db 447 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNGRITPKPSLLKAALIAGAADIGLGY 506
QY 301 PNGNOGWGRVTLDKSLNVAIVNNESSLSSTQKATYSFTATAGKPLKISLWSDAPASTTA 360
Db 507 PNGNOGWGRVTLDKSLNVAIVNNESSLSSTQKATYSFTATAGKPLKISLWSDAPASTTA 566
QY 361 SVTLVNDLDELVTAPNGTQVGNDEFTSPYNDNWDGRNNVENFINAPQSGTYYTIEVOAYN 420
Db 567 SVTLVNDLDELVTAPNGTQVGNDEFTSPYNDNWDGRNNVENFINAPQSGTYYTIEVOAYN 626
QY 421 VPVGPQTFLSIAVN 434
Db 627 VPVGPQTFLSIAVN 640
RESULT 11
ADM40773
ID ADM40773 standard; protein; 640 AA.
XX ADM40773;
AC ADM40773;
XX
DT 01-JUL-2004 (first entry)
XX
DE Alkaline protease from Bacillus sp. KSM-KP43.
XX
KW alkaline protease; laundry detergent; bleaching agent; detergent;
KW denture-cleaning agent; enzyme.
XX
OS Bacillus sp.; KSM-KP43.
XX
PN US2004072321-Al.
XX
PD 15-APR-2004.
XX
PF 09-JUN-2003; 2003US-00456479.
XX
PR 26-JUN-2002; 2002JP-00186387.
XX 18-OCT-2002; 2002JP-00304232.
XX (KAOS) KAO CORP.
XX
PI Sato T, Okuda M, Takimura Y, Sumitomo N, Nomura M, Kobayashi T;
XX
DR WPI; 2004-328572/30.
XX N-PSDB; ADM40772.
DR
PT New alkaline protease having a mutant prepro sequence where amino acid
PT residues at positions 52, 75 and 142 are substituted with another amino
PT acid residue, useful as enzyme component of laundry detergents, or

PT bleaching agents.

PS Disclosure; SEQ ID NO 4; 29pp; English.

XX

CC The invention relates to an alkaline protease having a prepro sequence.

CC The prepro sequence is a mutant sequence of SEQ ID NO: 1, or an amino acid sequence having 80% homology or higher to SEQ ID NO: 1, where amino acid residues at: (a) position 52 is substituted by aspartic acid or arginine; (b) position 75 is substituted by alanine or arginine; and (c) position 142 is substituted by lysine. The alkaline protease is useful as an enzyme which can be incorporated into laundry detergents, bleaching agents, detergents for cleaning hard surfaces or drainpipes, denture-cleaning agents, and detergents for sterilising medical apparatus. The present sequence represents alkaline protease from *Bacillus* sp. KSM-KP43.

XX

SQ Sequence 640 AA;

Query Match 99.6%; Score 2242; DB 8; Length 640;

Best Local Similarity 99.8%; Pred. No. 2.6e-159;

Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIKVADVAQHSYGLYGQGI VAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 60

DB |||||

QY 207 NDVARGIKVADVAQHSYGLYGQGI VAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 266

DB |||||

QY 61 NANDTNGHGHVAGSVLGNSTKMGAPQANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120

DB |||||

QY 267 NANDTNGHGHVAGSVLGNSTKMGAPQANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 326

DB |||||

QY 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180

DB |||||

QY 327 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386

DB |||||

QY 181 TVGATENLRPSPGSGYADNINHVAFSSRGPTKDGRIKPDVMAPGTFILSARSLAPDSF 240

DB |||||

QY 387 TVGATENLRPSPGSGYADNINHVAFSSRGPTKDGRIKPDVMAPGTFILSARSLAPDSF 446

DB |||||

QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKRGITPKPSLLKAALIAGAADIGLY 300

DB |||||

QY 447 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKRGITPKPSLLKAALIAGAADIGLY 506

DB |||||

QY 301 PNGNCGWRVTLDKSLNVAYNNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360

DB |||||

QY 507 PNGNCGWRVTLDKSLNVAYNNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 566

DB |||||

QY 361 SVTLVNDLVLITAPNGTOYVGNDFTPSYNDNWDGNNVNFVFINAQSGTGTITIEVQAYN 420

DB |||||

QY 567 SVTLVNDLVLITAPNGTOYVGNDFTPSYNDNWDGNNVNFVFINAQSGTGTITIEVQAYN 626

DB |||||

QY 421 VPVGPOTFSLAIVN 434

DB |||||

QY 627 VPVGPOTFSLAIVN 640

DB |||||

RESULT 12

ADS14437

ID ADS14437 standard; protein; 640 AA.

XX

AC ADS14437;

DT

DT 30-DEC-2004 (first entry)

XX

DE *Bacillus* alkaline protease KP43.

XX

XX protease; enzyme; alkaline protease; laundry detergent; KP43.

XX

OS *Bacillus* sp.; KSM-KP43.

XX

XX Key Location/Qualifiers

FT Peptide 1..206

FT Protein 207..640

XX

PN EP1466962-A1.

XX 13-OCT-2004.

XX

PF 08-APR-2004; 2004EP-00008604.

XX

PR 10-APR-2003; 2003JP-00106709.

XX

PA (KAOS) KAO CORP.

XX

PI Okuda M, Sato T, Takimura Y, Sumitomo N, Kobayashi T;

XX

XX WPI; 2004-711313/70.

DR N-P8DB; ADS14428.

XX

PT New engineered alkaline protease, useful particularly in laundry

PT detergents, comprising specified amino acids at particular positions.

XX

PS Disclosure; SEQ ID NO 1; 31pp; English.

XX

CC The invention relates to a novel alkaline protease. The new alkaline protease comprises an amino acid sequence in which one or more amino acid residues selected from those located at 7 specific positions within ADS14427, or at positions corresponding to these positions are: position 15 (thiethidine), position 16 (threonine or glutamine), position 166 (glycine), position 167 (valine), position 187 (serine), position 346 (arginine), and position 405 (aspartic acid). The alkaline protease is useful in industry particularly in laundry detergents, but also e.g. in fibre modifying agents, leather processing agents, cosmetic compositions, bath additives, food-modifying agents, and pharmaceuticals. The present sequence represents the wild-type *Bacillus* sp. KSM-KP43 alkaline protease, KP43. The sequence is shown in the sequence listing as part of SEQ ID NO:1

XX

SQ Sequence 640 AA;

Query Match 99.6%; Score 2242; DB 8; Length 640;

Best Local Similarity 99.8%; Pred. No. 2.6e-159;

Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIKVADVAQHSYGLYGQGI VAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 60

DB |||||

QY 207 NDVARGIKVADVAQHSYGLYGQGI VAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 266

DB |||||

QY 61 NANDTNGHGHVAGSVLGNSTKMGAPQANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120

DB |||||

QY 267 NANDTNGHGHVAGSVLGNSTKMGAPQANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 326

DB |||||

QY 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180

DB |||||

QY 327 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386

DB |||||

QY 181 TVGATENLRPSPGSGYADNINHVAFSSRGPTKDGRIKPDVMAPGTFILSARSLAPDSF 240

DB |||||

QY 387 TVGATENLRPSPGSGYADNINHVAFSSRGPTKDGRIKPDVMAPGTFILSARSLAPDSF 446

DB |||||

QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKRGITPKPSLLKAALIAGAADIGLY 300

DB |||||

QY 447 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKRGITPKPSLLKAALIAGAADIGLY 506

DB |||||

QY 301 PNGNCGWRVTLDKSLNVAYNNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360

DB |||||

QY 507 PNGNCGWRVTLDKSLNVAYNNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 566

DB |||||

QY 361 SVTLVNDLVLITAPNGTOYVGNDFTPSYNDNWDGNNVNFVFINAQSGTGTITIEVQAYN 420

DB |||||

QY 567 SVTLVNDLVLITAPNGTOYVGNDFTPSYNDNWDGNNVNFVFINAQSGTGTITIEVQAYN 626

DB |||||

QY 421 VPVGPOTFSLAIVN 434

DB |||||

QY 627 VPVGPOTFSLAIVN 640

DB |||||

RESULT 13

ADT49613	ID	ADT49613 standard; protein; 641 AA.
XX	AC	ADT49613;
XX	DT	30-DEC-2004 (first entry)
XX	DE	Bacillus alkaline protease.
XX	KW	Alkaline protease; detergent; fiber modification; leather processing; cosmetic; bath additives; food-modification; pharmaceutical; enzyme.
XX	OS	Bacillus sp. KSM-KP43.
XX	FH	Key Location/Qualifiers
FT	Peptide	1..206
FT	Protein	/note= "signal peptide"
FT	Protein	207..641
XX	FT	/note= "specifically claimed mature protein (SEQ ID 1)"
XX	PN	EPI466970-A1.
XX	PD	13-OCT-2004.
XX	PF	08-APR-2004; 2004EP-00008605.
XX	PR	10-APR-2003; 2003JP-00106708.
XX	PA	(KAOS) KAO CORP.
XX	PI	Sato T, Okuda M, Koyama S, Izawa Y, Kobayashi T;
XX	DR	WPI; 2004-711317/70.
XX	N-PSDB:	ADT49605.
XX	PT	New engineered alkaline protease with improved activity and thermal stability, useful particularly in detergents such as laundry detergents.
XX	PS	Disclosure; Page 19-25; 35pp; English.
XX	CC	The invention relates to an alkaline protease and its encoding gene. The alkaline protease can be expressed by standard recombinant methodology. The alkaline protease is useful in the industry particularly in detergents such as laundry detergents, but also in fiber modifying agents, leather processing agents, cosmetic compositions, bath additives, food-modifying agents, and pharmaceuticals. The enzyme has good activity and thermal stability. The present sequence represents an alkaline protease from Bacillus sp. KSM-KP43.
XX	SQ	Sequence 641 AA;
XX	Query Match	99.6%; Score 2242; DB 8; Length 641;
XX	Best Local Similarity	99.8%; Pred. No. 2.6e-159;
XX	Matches 433; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Qy	1	NDVARGIVKADVAQAHSYGLYGQGQIVAVADTGTDGRNDSMHEAFRGKITALVALGRTN 60
Db	207	NDVARGIVKADVAQAHSYGLYGQGQIVAVADTGTDGRNDSMHEAFRGKITALVALGRTN 266
Qy	61	NANDTNHGTHVAGSVLNGSTNKGMAPAQNLFVQSIMDSGGGLGSLPSNLQTLSQAYS 120
Db	267	NANDTNHGTHVAGSVLNGSTNKGMAPAQNLFVQSIMDSGGGLGSLPSNLQTLSQAYS 326
Qy	121	AGARIHTNSGKAVNGAYTTDSNRVDVYVRKNDMTILFAAGNEGPGGTISAPGTAKNAI 180
Db	327	AGARIHTNSGKAVNGAYTTDSNRVDVYVRKNDMTILFAAGNEGPGGTISAPGTAKNAI 386
Qy	181	TVCATENLPSPFGSYADNINHVAQFSRRGPTKDGRIKPDVMAPGTFILSARSSLPDSSF 240
Db	387	TVCATENLPSPFGSYADNINHVAQFSRRGPTKDGRIKPDVMAPGTFILSARSSLPDSSF 446
Qy	241	WANHDSKYAMCGTSMATPIVAGNVAQLREHFVKVRGITTPKPSLLKAALIAGAADIIGLY 300

CC information given in Example 1.

XX Sequence 434 AA;

Query Match 99.5%; Score 2239; DB 8; Length 434;
Best Local Similarity 99.3%; Pred. No. 2.6e-159;
Matches 431; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRN 60
DB 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRN 60

QY 61 NANDTNGHGTGVAGSVLGNSTKMGAPQANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGTGVAGSVLGNSTKMGAPQANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120

QY 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180

QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAPGTFILSARSLAPDSF 240
DB 181 TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAPGTFILSARSLAPDSF 240

QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKRGIPTPKPSLLKAALIAGAADIGLY 300
DB 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKRGIPTPKPSLLKAALIAGAADIGLY 300

QY 301 PNGNGQWGRVTLDKSLNVAIYVNESSLSSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
DB 301 PNGNGQWGRVTLDKSLNVAIYVNESSLSSTSQKATYSFTATAGKPLRISLVWSDAPASTTA 360

QY 361 SVTLVNDLDLVTAPNGTQYVGNDFTS PYNDNWDGRNNVNFVINAPOS GTTYTIEVQAYN 420
DB 361 SVTLVNDLDLVTAPNGTQYVGNDFTS PYNDNWDGRNNVNFVINAPOS GTTYTIEVQAYN 420

QY 421 VPVGPQTFSLAIVN 434
DB 421 VPVGPQTFSLAIVN 434

RESULT 15
ADM40780
ID ADM40780 standard; protein; 434 AA.
XX ADM40780;
AC ADM40780;

XX 01-JUL-2004 (first entry)
DE Alkaline protease #2 from Bacillus sp. KSM-KP9865.
XX alkaline protease; laundry detergent; bleaching agent; detergent;
KW denture-cleaning agent; enzyme.

OS Bacillus sp.; KSM-KP9865.

XX US2004072321-A1.

XX 15-APR-2004.

XX 09-JUN-2003; 2003US-00456479.

XX 26-JUN-2002; 2002JP-00186387.

XX 18-OCT-2002; 2002JP-00304232.

XX (KAOS) KAO CORP.

XX Sato T, Okuda M, Takimura Y, Sumitomo N, Nomura M, Kobayashi T;

XX WPI; 2004-328572/30.

XX New alkaline protease having a mutant prepro sequence where amino acid

PT residues at positions 52, 75 and 142 are substituted with another amino

PT acid residue, useful as enzyme component of laundry detergents, or
XX bleaching agents.

PS Disclosure; SEQ ID NO 11; 29pp; English.

XX The invention relates to an alkaline protease having a prepro sequence.
CC The prepro sequence is a mutant sequence of SEQ ID NO: 1, or an amino
CC acid sequence having 80% homology or higher to SEQ ID NO: 1, where amino
CC acid residues at: (a) position 52 is substituted by aspartic acid or
CC arginine; (b) position 75 is substituted by alanine or arginine; and (c)
CC position 142 is substituted by lysine. The alkaline protease is useful as
CC an enzyme which can be incorporated into laundry detergents, bleaching
CC agents, detergents for cleaning hard surfaces or drainpipes, denture-
CC cleaning agents, and detergents for sterilising medical apparatus. The
CC present sequence represents an alkaline protease used in homology
CC comparison with alkaline protease from Bacillus sp. KSM-KP43.

XX Sequence 434 AA;

Query Match 99.4%; Score 2237; DB 8; Length 434;
Best Local Similarity 99.5%; Pred. No. 3.6e-159;
Matches 432; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRN 60
DB 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRN 60

QY 61 NANDTNGHGTGVAGSVLGNSTKMGAPQANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGTGVAGSVLGNSTKMGAPQANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120

QY 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
DB 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180

QY 181 TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAPGTFILSARSLAPDSF 240
DB 181 TVGATENLRPSFGSYADNINHVAQFSRGPTKDGRIKPDVMAPGTFILSARSLAPDSF 240

QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKRGIPTPKPSLLKAALIAGAADIGLY 300
DB 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKRGIPTPKPSLLKAALIAGAADIGLY 300

QY 301 PNGNGQWGRVTLDKSLNVAIYVNESSLSSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
DB 301 PNGNGQWGRVTLDKSLNVAIYVNESSLSSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360

QY 361 SVTLVNDLDLVTAPNGTQYVGNDFTS PYNDNWDGRNNVNFVINAPOS GTTYTIEVQAYN 420
DB 361 SVTLVNDLDLVTAPNGTQYVGNDFTS PYNNNWDGRNNVNFVINAPOS GTTYTIEVQAYN 420

QY 421 VPVGPQTFSLAIVN 434
DB 421 VPVGPQTFSLAIVN 434

Search completed: April 7, 2006, 09:29:28
Job time : 95 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 7, 2006, 09:32:05 ; Search time 25 Seconds
(without alignments)
1670.323 Million cell updates/sec

Title: US-10-820-714A-1-HIS15
Perfect score: 2251
Sequence: 1 NDVARGIVKADVAQHSYGLY.....EVQAYNPVPGQTFSIAIVN 434

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	523.5	23.3	1743	2 T18279	multidrug resist
2	497	22.1	1905	2 T18267	multidrug resist
3	347.5	15.4	444	2 B83891	intracellular alka
4	320.5	14.2	442	2 A69587	intracellular alka
5	310.5	13.8	806	2 A41341	microbial serine p
6	302.5	13.4	1398	2 T28159	pyrolysin (EC 3.4.
7	283	12.6	580	2 S11890	serine proteinase
8	281	12.5	419	1 S25835	subtilisin (EC 3.4
9	280	12.4	799	2 G83753	subtilisin-type pr
10	279.5	12.4	1345	2 T29090	surface layer-asso
11	277	12.3	420	1 S23407	subtilisin (EC 3.4
12	267	11.9	715	2 JC4908	alkaline serine pr
13	261	11.6	1331	1 A72647	probable surface l
14	259.5	11.5	513	1 A35742	aqualyisin (EC 3.4.
15	259.5	11.5	757	2 C84120	subtilisin-type pr
16	253.5	11.3	894	2 F69730	cell wall-associat
17	251	11.2	627	2 D75393	serine proteinase,
18	248.5	11.0	380	2 A49778	high-alkaline seri
19	246.5	11.0	402	1 JU0332	alkaline proteinas
20	246.5	11.0	534	1 JS0173	alkaline proteinas
21	244.5	10.9	382	1 SUBSN	subtilisin (EC 3.4
22	242.5	10.8	519	2 S71451	halolyisin R4 (EC 3
23	241.5	10.7	401	2 I35974	serine proteinase
24	240	10.7	488	2 A11930	proteinase [import
25	235	10.4	382	2 JH0780	subtilisin (EC 3.4
26	234.5	10.4	381	2 JH0778	subtilisin (EC 3.4
27	234	10.4	378	2 A33973	high-alkaline seri
28	234	10.4	910	2 C69456	subtilisin sendai
29	234	10.4	1374	2 D72593	hypothetical prote

30	232.5	10.3	381	1 SUBSI	subtilisin (EC 3.4
31	232.5	10.3	381	1 SUBSS	subtilisin (EC 3.4
32	232.5	10.3	381	2 JQ1487	subtilisin (EC 3.4
33	232.5	10.3	525	2 G84406	halolyisin [importe
34	231	10.3	321	1 S27501	alkaline proteinas
35	230.5	10.2	272	2 A23624	subtilisin (EC 3.4
36	229.5	10.2	379	1 SUBSCL	subtilisin (EC 3.4
37	229.5	10.2	601	2 JC4576	serine proteinase
38	227	10.1	1167	1 A35066	streptococcal C5a
39	226.5	10.1	1118	2 H97298	subtilisin like pr
40	225.5	10.0	1052	2 T17093	intraluminal subti
41	224	10.0	613	2 S75976	hypothetical prote
42	223.5	9.9	361	2 A48373	high-alkaline seri
43	221.5	9.8	275	2 JC1085	subtilisin (EC 3.4
44	221.5	9.8	261	2 G83756	subtilisin-type al
45	221.5	9.8	530	2 A42605	halolyisin (EC 3.4.

ALIGNMENTS

RESULT 1

Ti8279
multidrug resistance transport protein - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18279
R:Shaulsky, G.; Loomis, W.F.
Submitted to the EMBL Data Library, June 1996
A:Reference number: Z18855
A:Accession: T18279
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1743 <SHA>
A:Cross-references: UNIPROT:Q23868; UNIPARC:UPI000013687D; EMBL:U60086; NID:gl399914; PIR
C:Genetics:
A:Gene: tagC

Query Match 23.3%; Score 523.5; DB 2; Length 1743;
Best Local Similarity 27.9%; Pred. No. 2.9e-25;
Matches 165; Conservative 81; Mismatches 150; Indels 195; Gaps 24;

Qy	19	LYGQGIIVAVADTGLDTGR	-----NDS-----SMHEAPRGKITALYALGRTNNANDTNGH	68
Db	314	LRKGQILSIADTGLDGHCFSDSKYPIPLNSVNLNR	-KVVTYITTSDDSDKVDGH	372
Qy	69	GTHVAGSVLG	-----NGSTNKGMAPQANLVFQSIMDSGGGLGL--PSNLTQLFSQAY	119
Db	373	GTHICGSAAGTPEDSSVNISSPFGSLATDAKIAF	---FDLASGSSSILTPFSDLKQLYQPLY	429
Qy	120	SAGARIHNSWGA	----AVNGAYTTDSRNVDDYVRKN-DMTILFAAGNEGNGGTIS--A	172
Db	430	DAGARVHCDSMGVSVEGTGYSDTASIDDFLTFHPDFIILRAAGN	---NEQVLSLTL	486
Qy	173	PCTAKNAITVGATENLR	-----PSFGSYADNI-----	199
Db	487	QSTAKNVITVGAHQTHENYLTGDNINYQSSVDINQELICDFSRYCNYTTAQCLLES	546	
Qy	200	-----NHVAQFSRGTQDKGRIKPDVMAQGTFL	228	
Db	547	NATTGLASCCPTLLRKSVIDAANTQPLLNVENNICSFSKSGPTHGDMKPAALVAPGEYIT	606	
Qy	229	SARSSLA	-----PDSSFWANHDSKYVYGGTSMATPIVAGNVAQLREH-----F	272
Db	607	SARSGNANTTDCQGDGSL-PNTNALLA-ISGTSWATSFAAAATILRQYLDVGYPTGSI	664	
Qy	273	VKNRGITPKPSLLKAALAGA	-----ADIGLYPNGN-----QGWGRVT	311
Db	665	VESNKLQPTGSLKALMINNAQLNGTQTITSSITYPSNVQVFENFAGASLVQGWGAIR	724	
Qy	312	LKSLNVAYNESS	-----SLTSQATYSFT--	338
Db	725	MSNWLHVNNNNNNNNNTKSDGITKFDGIGGLDLRLVKPNQWKESLSLTGQNTSYCTYK	784	

A;Residues: 1-442 <KUN>
A;Cross-references: UNIPROT:O31788; UNIPARC:UPI000006043F; GB:Z99113; GB:AL009126; NID:9
A;Experimental source: strain 168
C;Genetics:
F;146-398/Domain: subtilisin homology <SBT>
Query Match 14.2%; Score 320.5; DB 2; Length 442;
Best Local Similarity 29.7%; Pred. No. 3.9e-13;
Matches 107; Conservative 50; Mismatches 104; Indels 99; Gaps 16;
QY 11 DVAQHSYGLYGQCOQIVAVADTGLTGRNDSMHEAPRGKITALYALGRTNAN-----D 64
DB EVVRNQTLTGKVTAVVDTGI-----YHPDLEGR-----IGFADVMNQKTEPYD 183
QY 65 TNGHGTHTVAGSVLNGSTN-----KGMAPQANLVFQSIMDSGGGLGSLPNLQTLFSGQAYS 120
DB DNGHGTHTVAGSVLNGSTN-----KGMAPQANLVFQSIMDSGGGLGSLPNLQTLFSGQAYS 120
QY 121 AGARIHTNSWGAIVN-----GAYTDSRNVDYVYKND-----MTIL 157
DB -----EWCIQYNEPDPEIDIMMSLGGDALRYDHEQEDPLVRAVEEAWAGIVVC 288
QY 158 FAAGNEPNGGTTASPTAKNAITVGCATENLRPSFGSYADNINHVAOFSRSGPTKDGRIK 217
DB VAAGNSGPOSQTASPGVSEKVIITVGALDNNNTA-----SSDDTVAASFSGRPTVVGREK 344
QY 218 PDVMAPTGPTILSARSLAPDSSP-----WANHDSKYAYMGGTSMATPIVAGNVAQLREHF 272
DB PDILAPGVNIIISLR-----PNSYIDKLQKSRVSGSQVFTSGTSMATPICAGIAALIQL-- 399
QY 273 VKNRGITPK--PSLLKAAIAGAADIGLVPGNQGWGRVTLDKSLNV---AYVNESSSL 327
DB -QNPDLTPEDEVKELLK-----NGTDKW-----KDEDPNIIYGAGVNAENSV 439
RESULT 5
A41341
Microbial serine proteinase (BC 3.4.21.-), minor (vpr), precursor - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 17-Jul-1992 #sequence revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: A41341; B41341; S39730; D69730
R;Sloma, A.; Rufo Jr., G.A.; Theriault, K.A.; Dwyer, M.; Wilson, S.W.; Pero, J.
J. Bacteriol. 173, 6889-6895, 1991
A;Title: Cloning and characterization of the gene for an additional extracellular serine
A;Reference number: A41341; MUID:92041574; PMID:1938892
A;Accession: A41341
A;Molecule type: DNA
A;Residues: 1-806 <SLO>
A;Cross-references: UNIPROT:P29141; UNIPARC:UPI0000060C20; GB:M76590; NID:G143819; PIDN:
A;Accession: B41341
A;Molecule type: protein
A;Residues: 161-195 <SL2>
A;Cross-references: UNIPARC:UPI0000178D67
R;Glaser, P.; Kunst, F.; Arnaut, M.; Coudart, M.P.; Gonzales, W.; Hullo, M.F.; Ionescu,
A.; Rapoport, G.; Danchin, A.
Mol. Microbiol. 10, 371-384, 1993
A;Title: Bacillus subtilis genome project: cloning and sequencing of the 97 kb region fr
A;Reference number: S39655; MUID:95020537; PMID:7934828
A;Accession: S39700
A;Molecule type: DNA
A;Residues: 1-806 <GLA>
A;Cross-references: UNIPARC:UPI0000060C20; EMBL:X73124; NID:G413923; PIDN:CAAS1601.1; PI
R;Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruchi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holzapfel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maguda, S.; Mausel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, A.; Tosaoto, V.; Uchiyama,
I.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yamamoto, K.; Yata, K.; Yoshida, K.
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: D69730
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-806 <KUN>
A;Cross-references: UNIPARC:UPI0000060C20; GB:Z99123; GB:AL009126; NID:G2636240; PIDN:CAI
A;Experimental source: strain 168
C;Comment: The amino terminal sequence of the mature protein and a molecular weight of or
C;Genetics:
A;Gene: vpr
A;Start codon: TTG
C;Superfamily: microbial serine proteinase vpr; subtilisin homology
C;Keywords: hydrolase; serine proteinase
F;1-28/Domain: signal sequence predicted <SIG>
F;29-160/Domain: propeptide #status predicted <PRO>
F;180-548/Domain: subtilisin homology #status atypical <SBT>
Query Match 13.8%; Score 310.5; DB 2; Length 806;
Best Local Similarity 23.5%; Pred. No. 3.8e-12;
Matches 129; Conservative 58; Mismatches 157; Indels 205; Gaps 18;
QY 18 GLYGQCOQIVAVADTGLDTGR-----NDSSMHEAPRGKITALYALGRTN 60
DB 177 GVTGKGIKVAIITGVEYNHPLKKNFGQYKGVDFVNDYDPKETPTG-----D 225
QY 61 NANDTNGHGTHTVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGSLPNLQTLFSGQAYS 120
DB 226 PRGEATDGHGTHTVAGTVAANG-TIKGVAPDATLLAVRVLPGFG--SETTENVIAGVERAVQ 282
QY 121 AGARIHTNSWGAIVNCAVYTTDSRNVDYVYKNDMTILFAAGNEPNGGTTASPTAKNAI 180
DB 283 DGADVNNLSLNGSLNPNPWATSTAL-DWAMSEGVAVTSGNSGPNGTWVSGPTSGREAI 341
QY 181 TVGATE-----NURPSFGSY-----195
DB 342 SVGATQLPLNEYAVTFGSSYSSAKVMGYNKEDDVKALNNKEVELVEAGIGEAKDFEGKDLT 401
QY 196 -----ADNI-----199
DB 402 GKAVVYKRSIAFVDKADNAKAKAGIWMVYNNLSGEIEANVPGMSVPTIKLSLEGEKL 461
QY 200 -----NHVQFSSRGPTKD-GRIPKDVMAPTGTFILSARSLAP 236
DB 462 VSALKAGETKTTFKLTIVSKALGEQVADFSRSGFVMDTWIKPDISAPGVNIVSTIPTHDP 521
QY 237 DSSFVWANDSKYAYMGGTSMATPIVAGNVAQLREHFVQVRGITPKPSL--LKAALIAGAA 294
DB 522 D-----HPYGYGSKQGTSMASPHIAGAVAIKQ-----AKPKWSVEQIKAAIMNTAV 568
QY 295 DI-----GLGYPGNQGWGRVTLDKSLNVAYVNESSLTSQKATYSFTATAGKPLKISLV 350
DB 569 TLKDSDEGYEPHNAQAGSARI-----MNAIKADSLVSPGYSY----GTFLK---- 612
QY 351 WSDAPASTTASTVANDLDELVTAPNGTOYVGNDFSPYNDNDWG--RNNVENVFVINAQ 408
DB 613 -ENGNETKNETFTIENQ-----SSIRKSTYLEYSPNGSGISTSGTSRVRVIPAQ 660
QY 409 SGTYTIEVQ 417
DB 661 TCKATAKVK 669
RESULT 6
T28159
pyrolysin (EC 3.4.-.-) - Pyrococcus furiosus
C;Species: Pyrococcus furiosus
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28159

R:Voorthorst, W.G.B.; Eggen, R.I.L.; Geerling, A.C.M.; Platteeuw, C.; Siezen, R.J.; Vos, J. Biol. Chem. 271, 20426-20431, 1996
A:Title: Isolation and characterization of the hyperthermostable serine protease, pyroly
A:Reference number: Z20481; MUID:96355370; PMID:8702780

A:Accession: T28159
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1398 <VO>
A:Cross-references: UNIPROT:P72186; UNIPARC:UPI000016FD59; EMBL:U55835; NID:g1556462; PI
A:Experimental source: DSN3638
C:Genetics:
C:Keywords: hydrolase; serine proteinase

Query Match 13.4%; Score 302.5; DB 2; Length 1398;
Best Local Similarity 26.6%; Pred. No. 2.6e-11;
Matches 139; Conservative 57; Mismatches 178; Indels 149; Gaps 22;
QY 21 GOGQIVAVADTGLDTRNDSS-----SMHEAFRGKITALYALGRTNAN----- 63
DB 301 GNGYDIAYVDTLDYDFDEVPLGQYNYVDYDAVSYYGPLYNYLAEIDPNGEYAVFGW 360
QY 64 DTNGHGTHVAGSVLNGSTN-----KGMAPQAN 91
DB 361 DGHGHGTHVAGTVAGYDSNDAWDLMSYSGEWVFSRLYGYWDTYNTVTTDTVQGVAPGAQ 420
QY 92 LVFQSIMSGGLGLPSNLQTLFSQAYSAGARIHTNSWGAANGAYT--TDSRN--VDD 147
DB 421 INAIRVLR--DGRGSMWDIIEGM--TYAATHGADVISMSLGG--NAPYLDGTDPSVAVDE 476
QY 148 YVRKNDMTILFAAGNEGPNNGTISAPGTAKNAITVGATENLRPSFGSYAD----- 197
DB 477 LTEKGVVFPVIAAGNEGGINVSGFVATKAITVGAAA--VPINGVVYSQALGYPDYVG 535
QY 198 -----NINHVAOFSSRGPTKGRIPKPDVNPAGTIFILSARSLAPDSSFANHDSKYA 249
DB 536 FYYFPAYTNV--RIAFSSRGPRIDGEIKENVVAPGVYISLPMWIGGADF----- 585
QY 250 YNGGTSMTPIVAGNVQALREHFVKNRGIPTKPSLLKAALIAAADI-----GLYPNG 303
DB 586 -MSGTSMATPHVSGVALLISG--PKPEGIYYPNDIIRKLVESGATWLEGDPYTGOKYTEL 643
QY 304 NGWGRVTLDKSLNAVYVNESSLSSTSKATYSFTATAGKPLKISLVMSDAPASTTA--- 360
DB 644 DQGHGLVNVKSWEI-----LKAINGTTLPIVDHMADKYSDFAEYL 685
QY 361 SVTLVNDLVLITAPN-----GTQYVGN-----DFTSPYNDW-----DG-----RNNVNVF 403
DB 686 GVDVIRGLYARNIPDIVEMHKKYVGDTEYRTEIFYATEPWIKPFVSGSVILENNTEFVL 745
QY 404 -----INAPQSGTY-----TIEVQAYNVVPVGPQTF 429
DB 746 RVKYDVEGLEPLVGRRIIDPFTFVIEDEILNTVIVPEKFT 788

RESULT 7
S11890
serine proteinase (EC 3.4.21.-) precursor, extracellular - Xanthomonas campestris pv. ca
N:Alternate names: subtilisin-related proteinase
C:Species: Xanthomonas campestris pv. campestris
C:Date: 21-Nov-1993 #sequence_revision 07-Feb-1997 #text_change 31-Dec-2004
R:Jiu, Y.N.; Tang, J.L.; Clarke, B.R.; Dow, J.M.; Daniels, M.J.
Mol. Gen. Genet. 220, 433-440, 1990
A:Title: A multipurpose broad host range cloning vector and its use to characterise an e
A:Reference number: S11890; MUID:90251253; PMID:2187155
A:Molecule type: DNA
A:Residues: 1-580 <LIU>
A:Cross-references: UNIPROT:P23314; UNIPARC:UPI000012A398; EMBL:X51635; NID:g48533; PIDN
A:Experimental source: Xanthomonas campestris pv. campestris
A>Note: the sequence from Fig. 4 is inconsistent with that from Fig. 3 in having 205-Ala
C:Superfamily: extracellular alkaline serine protease precursor, Alteromonas type

C:Keywords: extracellular protein; hydrolase; serine proteinase
F:1-32/Domain: signal sequence #status predicted <SIG>
F:168-423/Domain: subtilisin homology <SBT>

Query Match 12.6%; Score 283; DB 2; Length 580;
Best Local Similarity 26.2%; Pred. No. 1.4e-10;
Matches 127; Conservative 55; Mismatches 147; Indels 156; Gaps 24;
QY 21 GOGQIVAVADTGL-----DTGRNDSMHEAFRGKITALYALGRTNAN----- 64
DB 168 GSGTVVAVIDGITSHADLNANILAGYDFISDAITARDGNGRDSNAADGDEGHWAAECCA 227

QY 65 -----TNGHGTHVAGSVLNGSTNKGMAPQ-----NLVFSQIMD 99
DB 228 GIPAASSSMHGTHVAGTVAAVTNNTTGVAGTAYGAKVFPVRVLGKCGGSLSDIAAIVWA 287
QY 100 SGGGLGLPSNLQ--TLFSQAYSAGARIHTNSWGAANGAYTTDSRNVDYVYRKNDMTIL 157
DB 288 SGGTVSGIPANANPAEIVNMSLGGGSGCSTTQON--AINGAVSRGT-----TVV 334
QY 158 FAAGNEGPNNGTISAPGTAKNAITVGATEN--LRPSFGSYADNINHVAQFSSRGPTKQGR 215
DB 335 VAAGNDANVSG--SLPANCANVIAVAATTSAGAKASYNFGTGI----- 377
QY 216 IKPDVNPAGTIFILSARSS--LAPDSSFANHDSKYAYMGTSMATPIVAGNVQALREHFV 273
DB 378 ---DVSAPGSSILSTLNSGTTTPGS-----ASYASYNGTSMASPHVAGVALVQS--V 425
QY 274 KNRGTPK--PSLLK--AALTAGAADIGLVPNGQGRVTLDKSLNAVYNESS----- 325
DB 426 APTALTPAAVETLLKNTARALPGAC-----SGCGGAGIVNADAATAVTA--INGSGGGG 477
QY 326 -----SLSTSOKATYSFTATAGKPLKISLVMSDAPASTTASVTL--VND 367
DB 478 GGNLTNGTNPVTGLGAATGAEINITYITVPAG-----SGTLVTTSGGSD 523
QY 368 LDLVI---TAPNGTOYVGNDEFTSPYNDNWDGRNNVNFVINAPOSGTGTIEVOAYNVPG 424
DB 524 ADLYVRAGSAPDTSAYT---CRPVRS-----GNAETCTITAP--SGTYVVRUKAYS----- 569
QY 425 POTFS 429
DB 570 --TFS 572

RESULT 8
S25835
subtilisin (EC 3.4.21.62) precursor - Bacillus sp. (strain TA41)
C:Species: Bacillus sp.
C:Date: 22-Nov-1993 #sequence_revision 20-Feb-1995 #text_change 05-Oct-2004
C:Accession: S25835
R:Davail, S.; Feller, G.; Narinx, E.; Gerday, C.
Gene 119, 143-144, 1992
A:Title: Sequence of the subtilisin-encoding gene from an antarctic psychrotroph Bacillu
A:Reference number: S25835; MUID:93012966; PMID:1398082
A:Accession: S25835
A:Molecule type: DNA
A:Residues: 1-419 <DAV>
A:Cross-references: UNIPARC:UPI00000BB77A; EMBL:X63533; NID:g40198; PIDN:CAA45096.1; PID:
C:Superfamily: Subtilisin; subtilisin homology
C:Keywords: extracellular protein; hydrolase; serine proteinase
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-110/Domain: propeptide #status predicted <PRO>
F:111-419/Product: microbial serine proteinase #status predicted <MAT>
F:135-373/Domain: subtilisin homology <SBT>
F:144,184,359/Active site: Asp, His, Ser #status predicted

Query Match 12.5%; Score 281; DB 1; Length 419;
Best Local Similarity 33.0%; Pred. No. 1.2e-10;
Matches 87; Conservative 38; Mismatches 97; Indels 42; Gaps 13;
QY 21 GOGQIVAVADTGLDTRNDSSMH--BAFRGKITALYALGR-----NNANDTNGHGHVAGSV 76

Db 135 GAGINIAVLDTGVTNHNHPLDLSNNVEQKD-----FTVGTNFTDNSCTDRQGHGTHVAGSA 189
Qy 77 LKNGSTNK---GMAPQANL-VFQSIWDSGGGLG-GLPSNLQTLFQSAQYAGARIHTN-SW 130
Db 190 LANGGTGSGVYGVYGAPEADLWAYKVLGDDGSGYADDIAEAIHAGDQATALTALNKKVINMSL 249
Qy 131 GAAVNGAYTTDSNRVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNALTVCATENLRP 190
Db 250 GSGGESSLIT---NAVYAYDKGVLLIAAAGNSGPKPGSIGYPGALUNAVAALENTIQ 306
Qy 191 SFGSYADNINHVAQFSRSGPTKDG-----RIKPDVMAFGTFTLSARSSLAPDSSFWANH 244
Db 307 N-GTY-----RVADFSRGRKHTAGDYVIQKGDVEISAFGAAYYST-----W-F 348
Qy 245 DSKYAYMGTSMATPIVAGNAQL 268
Db 349 DGYATISGTSMASPAAGLAARI 372

RESULT 9
G83753
subtilisin-type proteinase (EC 3.4.21.-) vpr precursor [similarity] - Bacillus haloduran
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: G83753
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: G83753
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-799 <STO>
A:Cross-references: UNIPROT:Q9KEM1; UNIPARC:UPI00000C39DC; GB:AP001510; GB:BA000004; NID
A:Experimental source: strain C-125
C:Genetics:
A:Gene: vpr
C:Superfamily: microbial serine proteinase vpr; subtilisin homology
C:Keywords: hydrolase; serine proteinase
F:1-29/Domain: signal sequence #status predicted <SIG>

Query Match 12.4%; Score 280; DB 2; Length 799;
Best Local Similarity 24.7%; Pred. No. 3.3e-10;
Matches 117; Conservative 50; Mismatches 135; Indels 172; Gaps 16;
Qy 18 GLYGQGIIVAVADTGLDTRGNDSSHEAFRGKITALYALGRTNANDT-----NGH 68
Db 171 GYTGEITVAIILDTGVDTYHPD--LVHAF-GDYKGWDFDNDNDPQETPPGPRGIEETH 227
Qy 69 GTHVAGSVLGNGSTNGKMAPQANLVFQSIWDSGGGLGGLPSNLQTLFQSAQYAGARIHTN 128
Db 228 GTHVAGTVAANGLI-KGVAFDANLLAYRVLGPGG--RGSTAGVIAGIERAVQDGADIMNL 284
Qy 129 SNGAAVNGAYTTDSNRVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNALTVCATENL 188
Db 285 SLGNTLNDPDFATSIAL-DWAAEGVAVTSNGNSGFNNWTVGSPGTSRDALSVGAT---- 340
Qy 189 RPSFGSY-----ADNINH----- 201
Db 341 RLPYNYKASVTSDDIDYADIMGFPSPDEILLELDGETYEYAFAGLKPQDPEGVDVE 400
Qy 202 ----- 201
Db 401 GKIALIVRGEIPFVEKAENAKAAGAVGAIYNNVAGVQPTVPLAIPITIMLSNEDGLKMR 460
Qy 202 -----VAQFSRSGPT-KDGRIKPDVMAFGTFTLSARSSLAPD 237
Db 461 NELENGQNTVTSIEPDKLVGETVADFSSRGPVMTWKIPDVSAAPGVAIVSTIPTHQPD 520
Qy 238 SSGFWANHDSKYAYMGTSMATPIVAGNAQLREHFVKNRGITPKPSLLKAAIAGAADT- 296
Db 521 DPT-----GYSGRQGSTMASPHVAGAAALLLEAH-PWGV-----DHVKAALMNTAENLV 569

Qy 297 ---GLGYPNGNOGWRVTLDKSLNAVYVNESSLSSTSQKATV-SFTATAGKPLK 346
Db 570 DENGNRYPHNTQAG-----SIRIVDAIESETLVTPGSHSPGTFYKRGKQVE 617

RESULT 10
T29090
surface layer-associated STABLE proteinase - Staphylothermus marinus
N:Alternate names: hyperthermostable proteinase
C:Species: Staphylothermus marinus
C>Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C:Accession: T29090
R:Mayr, J.; Lupas, A.; Kellermann, J.; Eckerskorn, C.; Baumeister, W.; Peters, J.
Curr. Biol. 6, 739-749, 1996
A:Title: A hyperthermostable protease of the subtilisin family bound to the surface layer
A:Reference number: Z20559; MUID:96385442; PMID:8793300
A:Accession: T29090
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1345 <MAY>
A:Cross-references: UNIPROT:Q54437; UNIPARC:UPI0000062778; EMBL:U57968; NID:gl374755; PII
A:Experimental source: strain F1
C:Function:
A:Description: probably serves an exodigestive function related to the organism's energy
A>Note: stoichiometric S-layer component

Query Match 12.4%; Score 279.5; DB 2; Length 1345;
Best Local Similarity 29.9%; Pred. No. 7.2e-10;
Matches 99; Conservative 45; Mismatches 106; Indels 81; Gaps 14;
Qy 46 FRGKITALVALGRNTNANDTNGHGHVA-----GSVL-----GNGSTNK-GMAPQANLV 93
Db 445 YQGRVYAL-----VSDFHGHTGSVATVIASRGRLVLDYGDGKLYRIMGVAPGAKI- 495
Qy 94 FQSIWDSGGGLGGLPSNLQTLFQSAQYAG-----EAWLAGFNIVTSEEDGVVYLSLDPFGPHRADISNSW 546
Db 496 -----AGGDALLGNILVL--EAWLAGFNIVTSEEDGVVYLSLDPFGPHRADISNSW 546
Qy 131 GAAVNGAYTTDSNRVD-----DYVRKNDMTILFAAGNEGPNGGTISAPGTAK 177
Db 547 GSIYINFWLQPPGIDYRSSFMDEILAIRNYLIDGHVTIVFAAGNEGPGYSSNGAPGTGL 606
Qy 178 NAITVGATE-NLRPSFG---SYADNINHVAOFSSRGPTKDGRIKPDVMAFGTFTLSARS 232
Db 607 LVITAGASTLWDTYRIYGYPEGYAD---EVIFFSRSGPTGGQGYPKPDIVNIGAFEWASTR 663
Qy 233 SLAPDSSFWANHDSKYAYMGTSMATPIVAGNAQLREHFVKNRGITPKPSLLKAAIAG 292
Db 664 TI-DGRGYCAQPD---VFGGTSEATPYTSGTLALVFOAYKEVYNTTTPDPVTAKIILKSS 718
Qy 293 AADIGLYPNNGQWGRVTLDKSLNAVYVNE 323
Db 719 AKDI--WYPAFQSGSRVDALKAAADTVFISE 747

RESULT 11
S23407
subtilisin (EC 3.4.21.62) 1 precursor - Bacillus sp. (strain TA39)
C:Species: Bacillus sp.
C>Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 05-Oct-2004
C:Accession: S23407
R:Narinx, R.; Davail, S.; Feller, G.; Gerday, C.
Biochim. Biophys. Acta 1131, 111-113, 1992
A:Title: Nucleotide and derived amino acid sequence of the subtilisin from the antarctic
A:Reference number: S23407; MUID:92256481; PMID:1581352
A:Accession: S23407
A:Molecule type: DNA
A:Residues: 1-420 <NAR>
A:Cross-references: UNIPROT:P28842; UNIPARC:UPI0000136183; EMBL:XG2369; NID:g40200; PIDN:
C:Genetics:
A:Gene: sub1
C:Superfamily: Subtilisin; subtilisin homology
C:Keywords: extracellular protein; hydrolase; serine proteinase

Db 739 STSVYENVYSLLS-----GYSYFPLAPNPVEDQIYPGVLKPGETAVETVLKTL 788
RESULT 14
A35742
aqualysin (EC 3.4.21.-) I precursor - Thermus aquaticus
C:Species: Thermus aquaticus
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 05-Oct-2004
C:Accession: A35742; S00620; S00324
R:Terada, I.; Kwon, S.T.; Miyata, Y.; Matsuzawa, H.; Ohta, T.
J. Biol. Chem. 265, 6576-6581, 1990
A:Title: Unique precursor structure of an extracellular protease, aqualysin I, with NH-2
A:Reference number: A35742; MUID:90216674; PMID:2182621
A:Accession: A35742
A:Molecule type: DNA
A:Residues: 1-513 <TER>
A:Cross-references: UNIPROT:P08594; UNIPARC:UPI0000125D0A; GB:D90108; GB:J054
A:Note: the authors translated the codon CTG for residue 470 as Val, and GGT for residue
R:Kwon, S.T.; Terada, I.; Matsuzawa, H.; Ohta, T.
Eur. J. Biochem. 173, 491-497, 1988
A:Title: Nucleotide sequence of the gene for aqualysin I (a thermophilic alkaline serine
A:Reference number: S00620; MUID:88225062; PMID:3286255
A:Accession: S00620
A:Molecule type: DNA
A:Residues: 75-442 <KWO>
A:Cross-references: UNIPARC:UPI0000170448; EMBL:X07734; NID:G48069; PIDN:CAA30559.1; PID
A:Note: part of this sequence, including the amino and carboxyl ends of the mature prote
R:Matsuzawa, H.; Tokugawa, K.; Hamaoki, M.; Mizoguchi, M.; Taguchi, H.; Terada, I.; Kwon
Eur. J. Biochem. 171, 441-447, 1988
A:Title: Purification and characterization of aqualysin I (a thermophilic alkaline serin
A:Reference number: S00324; MUID:88151937; PMID:3162211
A:Accession: S00324
A:Molecule type: protein
A:Residues: 128-170 <MATS>
A:Cross-references: UNIPARC:UPI0000172C23
A:Superfamily: subtilisin; subtilisin homology
C:Keywords: extracellular protein; hydrolase; serine proteinase
F:1-14/Domain: signal sequence #status predicted <SIG>
F:15-127/Domain: propeptide #status predicted <PRO>
F:128-408/Product: aqualysin I #status experimental <MAT>
F:157-364/Domain: subtilisin homology <SBT>
F:255-257, 281-283/Region: S1 specificity crevice #status predicted
F:409-513/Domain: carboxyl-terminal propeptide #status predicted <CPR>
F:166,197,349/Active site: Asp, His, Ser #status predicted
Query Match 11.5%; Score 259.5; DB 1; Length 513;
Best Local Similarity 25.9%; Pred. No. 3.7e-09;
Matches 117; Conservative 45; Mismatches 144; Indels 145; Gaps 23;
QY 15 HSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALLY-ALGRNTNANDTNGHGHVHA 73
DB 151 YTVATGTRGVNVVVDITGRT-----THREFGRRARVGYDALG--GNQDNCNGHGHVHA 202
QY 74 GSVLNGSTNGKMAPQANLVFQSIMD--SGGGLGLPSNLQTLFSAQYSAGARIHTN--- 128
DB 203 GTI---GGVTYGVAKAVNLVYRVLDNCNGSGSTSGVIAGVDWV-----TRNHRRAV 251
QY 129 ---SMGAENVAGYTTDSRVNDDYVRKN---DMTILFAAGNEGPNGGTISAPGTAKNAITV 182
DB 252 ANKSLGGGVSTA-----LDNAVKNISIAAGVVVYVAAAGNDIANNACNYS- PARVAELIV 303
QY 183 GAT--ENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTIFLSARSLAPDSSF 240
DB 304 GATTSSDARASFNSYSCV-----DLFAPGASIPSA----- 334
QY 241 WANHDSKYAYMGGTSNATPIVAGNVAQLREHFVKNRGITP---KPSLLKAALIAGAADIG 297
DB 335 WYTSDTATQTLNGTSMATHPVAG-VAAL---YLEQNPSPASPASVAILNGATTGRLSGIG 391
QY 298 LGVPNGNCGWRVTLDKSLNVAVYVNESSLSSTSQATYSFTATAGPKPLKSLVWSDAPAS 357
DB 392 SGSPN-----RLLYSLLSSGS-----GSTAPCT 414

QY 358 T-----TASVTLVNDLVLITANGTQY-----VGNDFTSFYNDNDWGN-- 397
DB 415 SCSTYTGSLSGDGYNF---QPNGTYYYSAGTHRAWLRGPGAGTDF-DLYLWRWDGSRWL 470
QY 398 -----NVENVFINAPQSGTYTIEVQAYN 420
DB 471 TVGSSNGPTSEESLSYSGTAGYVLRWRYAYS 501
RESULT 15
C84120
subtilisin-type proteinase (EC 3.4.21.-) BH3763 precursor [similarity] - Bacillus halodurans
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence revision 01-Dec-2000 #text_change 09-Jul-2004
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512592; PMID:11058132
A:Accession: C84120
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-757 <STO>
A:Cross-references: UNIPROT:Q9K6G6; UNIPARC:UPI00000C42C2; GB:AP001519; GB:BA000004; NID
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH3763
C:Superfamily: microbial serine proteinase vpr; subtilisin homology
C:Keywords: hydrolase; serine proteinase
F:1-20/Domain: signal sequence #status predicted <SIG>
Query Match 11.5%; Score 259.5; DB 2; Length 757;
Best Local Similarity 22.6%; Pred. No. 6.3e-09;
Matches 119; Conservative 58; Mismatches 155; Indels 195; Gaps 20;
QY 8 VKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRG-----KITALYALG 57
DB 119 VRGMLDEEGVHLTGKGVAVVDTGIDYTHPD--LQSSYKGYDFVDYDDPMETTASQG 176
QY 58 RTNNANDTNGHGHVAGSVLNGSTNGKMAPQANLVFQSIMDSGGGLGLPSNLQTLFSG 117
DB 177 -----PPTLHGTSHVGIIAANGQV-KGVAPAEIYAVRALPGG--QGTTEQVIAIEK 227
QY 118 AVSAGARIHTNSGAAVNGAYTTDSRVNDDYVRKNDMTILFAAGNEGPNGGTISAPGTAK 177
DB 228 AVEDGVDVINLSLGNVTNGPDWPTSLADAAVEEGVAVT-SNGNSGPNMTVGSPTGSK 286
QY 178 NAITVGAT-----EN---LRPSFGS----- 194
DB 287 KAISVGASAPPLNTPLYTAFGENEISLYPFSGGLPWFAPKRDLPMDVGVGTEKEWEGVD 346
QY 195 -----YADNINH----- 201
DB 347 AEGKVLIKRGMVPTKVMHAAKARCVIINNTPGPTGMIEGVNIPVVSITREDG 406
QY 202 -----VAQFSSRG- TKDGRIKPDVMAPGTIFLSARSS 233
DB 407 EFLLEOLELQKNKELTLRTYRKEEDFVALFSSRGSPVTHTDVDPDVAVGVS1-----DS 462
QY 234 LAPDSSFWANHDSKYAYMGGTSNATPIVAGNVAQLREHFVKNRGITPK--PSLLKAALIA 291
DB 463 TTPNG-----YLGNGTSMAPHPVAGAAALIKQ-----AHPEWTPQVKAALMN 507
QY 292 GAADI---GLGYPNGNCGWRVTLDKSLNVAVYVNESSLSSTSQATYSFTATAGPKPKI 347
DB 508 TAKKLVQEGVPHETHEQGAGRIQVDKAV-----AATSLVYFGALSFGK---- 551
QY 348 SLVWSDAPASTTASVTL-VNDLVLITANGTQYVGNDFTSFYNDNDW 393
DB 552 ---WSKDDLRKRPVTLTIENHDTV---KRTYHISPPDPDVGVEW 591

Search completed: April 7, 2006, 09:32:40
Job time : 28 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 7, 2006, 09:29:44 ; Search time 114 Seconds
(without alignments)
2685.959 Million cell updates/sec

Title: US-10-820-714A-1-HIS15

Perfect score: 2251

Sequence: 1 NDVARGIKADVQAHSYGLY.....EVQAYNPVPGPTFSIAIVN 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	2242	99.6	Q93UV9_9BACI	Q93UV9 bacillus sp
2	2237	99.4	Q76184_9BACI	Q76184 bacillus sp
3	2178	96.8	Q9AQR3_9BACI	Q9AQR3 bacillus sp
4	2138	95.0	Q9AQR0_9BACI	Q9AQR0 bacillus sp
5	1998.5	88.8	Q9AQR1_9BACI	Q9AQR1 bacillus sp
6	1994.5	88.6	Q9AQR4_9BACI	Q9AQR4 bacillus sp
7	1987.5	88.3	Q9AQR2_9BACI	Q9AQR2 bacillus sp
8	870.5	38.7	Q4NB18_9MICC	Q4NB18 arthrobacte
9	755.5	33.6	Q6MKR4_BDEBA	Q6MKR4 bdellovibri
10	734.5	32.6	Q4NVB5_9DELT	Q4NVB5 anaeromyxob
11	591	26.3	Q4HUY5_GIBZE	Q4HUY5 gibberella
12	580	25.8	Q747P6_GEOSL	Q747P6 geobacter s
13	531.5	23.6	Q54M84_DICDI	Q54M84 dictyosteli
14	523.5	23.3	Q8T9W1_DICDI	Q8T9W1 dictyosteli
15	511.5	22.7	Q8T9W1_DICDI	Q8T9W1 dictyosteli
16	497	22.1	1 TAGB DICDI	Q54M83 dictyosteli
17	497	22.1	1306 2	Q54M83 dictyosteli
18	447	19.9	1752 2	Q9GTN7_DICDI
19	425.5	18.9	1388 2	Q580L9_9TRYP
20	414	18.4	654 2	Q8U0C9_PYRFU
21	414	18.4	663 2	Q5J1Z5_PYRKO
22	401.5	17.8	561 2	Q8RBJ2_THETN
23	393	17.5	1239 2	Q9FBZ4_STRCO
24	381	16.9	430 2	Q8ENV1_OCEIH
25	376	16.7	1253 2	Q9FC06_STRCO
26	365	16.2	1102 2	P95684_STRAO
27	358.5	15.9	1208 2	Q82B14_STRAW
28	349	15.5	1245 2	Q9RL54_STRCO
29	347.5	15.4	444 2	Q9KBJ7_BACHD
30	346.5	15.4	1139 2	Q82139_STRAW
31	343.5	15.3	1105 2	Q8KKH6_streptomyce

32	340	15.1	442	2	Q5L3I5_GEOKA	Q5L3I5 geobacillus
33	338	15.0	412	2	Q9AER6_THEYO	Q9AER6 thermoaer
34	337	15.0	412	2	Q8RC68_THETN	Q8RC68 thermoaer
35	336	14.9	1294	2	Q5OHM7_STRSH	Q5OHM7 streptomyce
36	333	14.8	1237	2	Q8GGT4_STRAZ	Q8GGT4 streptomyce
37	332.5	14.8	442	2	Q65IP4_BACLD	Q65IP4 bacillus li
38	331	14.7	795	2	Q5NW24_9ARCH	Q5NW24 uncultured
39	327.5	14.5	435	2	Q8EMJ3_OCEIH	Q8EMJ3 oceanobacil
40	324.5	14.4	818	2	Q79CG3_BACSP	Q79CG2 bacillus sp
41	324.5	14.4	824	2	Q45464_BACSP	Q45464 bacillus sp
42	323.5	14.4	1220	2	Q9LOAO_STRCO	Q9LOAO streptomyce
43	320.5	14.2	442	2	Q31788_BACSU	Q31788 bacillus su
44	320.5	14.2	891	2	Q93635_THESU	Q93635 thermococcu
45	310.5	13.8	806	1	SUBV_BACSU	P29141 bacillus su

ALIGNMENTS

RESULT 1
Q93UV9_9BACI
ID Q93UV9_9BACI PRELIMINARY; PRT; 640 AA.
AC Q93UV9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Protease.
GN Name=PROF;
OS Bacillus sp. KSM-KP43.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=109322;
RN [1]_TaxID=109322;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KP43;
RA Itoh S., Saeki K.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB051423; BAB55674.2; -; Genomic_DNA.
DR PDB; 1WMD; X-ray; A=207-640.
DR PDB; 1WME; X-ray; A=207-640.
DR PDB; 1WMF; X-ray; A=207-640.
DR MEROPS; S08.123; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_Bact_C.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF04151; PPC; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 640 AA; 67991 MW; 4BBAF77E9D592C15 CRC64;

Query Match 99.6%; Score 2242; DB 2; Length 640;
Best Local Similarity 99.8%; Pred. No. 3.1e-138;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	NDVARGIKADVQAHSYGLYGGQIVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN 60		
Db	207	NDVARGIKADVQAHSYGLYGGQIVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN 266		
QY	61	NANDTNGHGHVAGSVLNGSTNKGMA PQANLVFQISIMDSGGGLGGLPSNLQTLFSQAYS 120		
Db	267	NANDTNGHGHVAGSVLNGSTNKGMA PQANLVFQISIMDSGGGLGGLPSNLQTLFSQAYS 326		
QY	121	AGARHTHSWGAENVGYTTDSRNVDYVYRKNDMTILFAAGNEGNNGGTISAPGTAKNAI 180		
Db	327	AGARHTHSWGAENVGYTTDSRNVDYVYRKNDMTILFAAGNEGNNGGTISAPGTAKNAI 386		
QY	181	TVGATENLRPSFGSYADNINHVAFQSSRGPTKDGRIKPDVMAFGTIFLSARSLAPDSSF 240		
Db	387	TVGATENLRPSFGSYADNINHVAFQSSRGPTKDGRIKPDVMAFGTIFLSARSLAPDSSF 446		

```
QY 241 WANHDSKYAYMGTSWATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
Db 447 WANHDSKYAYMGTSWATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 506
QY 301 PNGNGWGRVTLDKSLNAVYVNESSLSSTQKATYSFTATAGKPLKI SLVWSDAPASTTA 360
Db 507 PNGNGWGRVTLDKSLNAVYVNESSLSSTQKATYSFTATAGKPLKI SLVWSDAPASTTA 566
QY 361 SVTLVNDLVLITAPNGTQYVGNDFSTPYNDWNGRNNVNFVINAPOSQYTTIEVOAYN 420
Db 567 SVTLVNDLVLITAPNGTQYVGNDFSTPYNDWNGRNNVNFVINAPOSQYTTIEVOAYN 626
QY 421 VVPGQPTFSLAIVN 434
Db 627 VVPGQPTFSLAIVN 640
RESULT 2
ID Q76L84_9BACI PRELIMINARY; PRT; 640 AA.
AC Q76L84;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Protease.
OS Bacillus sp. KSM-9865.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=192495;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KSM-9865;
RA Okuda M., Saeki K., Kobayashi T.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB084155; BAC82522.1; -; Genomic_DNA.
DR HSSP; P00782; 1AQN.
DR SMR; Q76L84; 207-640.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_Bact_C.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF04151; PPC; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 640 AA; 67940 MW; 421F7A150FF2868F CRC64;
Query Match 99.4%; Score 2237; DB 2; Length 640;
Best Local Similarity 99.5%; Pred. No. 6.6e-138;
Matches 432; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 NDVARGIKVADVAQHSYGLYGQGI VAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 207 NDVARGIKVADVAQHSYGLYGQGI VAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 266
QY 61 NANDTNGHGHVAGSVLNGSTNGKMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 267 NANDTNGHGHVAGSVLNGSTNGKMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
Db 327 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 386
QY 181 TVGATENLRPSFGSVADNINHVAQFSRGPTKDGRIKPDVMAPGTIFLSARSLAPDSF 240
Db 387 TVGATENLRPSFGSVADNINHVAQFSRGPTKDGRIKPDVMAPGTIFLSARSLAPDSF 446
QY 241 WANHDSKYAYMGTSWATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
Db 447 WANHDSKYAYMGTSWATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 506
```

```
QY 301 PNGNGWGRVTLDKSLNAVYVNESSLSSTQKATYSFTATAGKPLKI SLVWSDAPASTTA 360
Db 507 PNGNGWGRVTLDKSLNAVYVNESSLSSTQKATYSFTATAGKPLKI SLVWSDAPASTTA 566
QY 361 SVTLVNDLVLITAPNGTQYVGNDFSTPYNDWNGRNNVNFVINAPOSQYTTIEVOAYN 420
Db 567 SVTLVNDLVLITAPNGTQYVGNDFSTPYNDWNGRNNVNFVINAPOSQYTTIEVOAYN 626
QY 421 VVPGQPTFSLAIVN 434
Db 627 VVPGQPTFSLAIVN 640
RESULT 3
ID Q9AQR3_9BACI PRELIMINARY; PRT; 639 AA.
AC Q9AQR3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Protease.
OS Name=PROA;
OS Bacillus sp. 9860.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=133778;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=9860;
RX MEDLINE=20568675; PubMed=1118284; DOI=10.1006/bbrc.2000.3931;
RA Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
RA Horikoshi K.;
RT "Novel oxidatively stable subtilisin-like serine proteases from
RT alkaliphilic Bacillus spp.: enzymatic properties, sequences, and
RT evolutionary relationships.";
RL Biochem. Biophys. Res. Commun. 279:313-319(2000).
DR EMBL; AB046403; BAB21266.2; -; Genomic_DNA.
DR HSSP; P00782; 1SUP.
DR SMR; Q9AQR3; 206-639.
DR MEROPS; S08.123; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_Bact_C.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF04151; PPC; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 639 AA; 68186 MW; 316AF6FFDBE4FF54 CRC64;
Query Match 96.8%; Score 2178; DB 2; Length 639;
Best Local Similarity 96.1%; Pred. No. 4.8e-134;
Matches 417; Conservative 13; Mismatches 4; Indels 0; Gaps 0;
QY 1 NDVARGIKVADVAQHSYGLYGQGI VAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 206 NDVARGIKVADVAQHSYGLYGQGI VAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 265
QY 61 NANDTNGHGHVAGSVLNGSTNGKMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 266 NANDTNGHGHVAGSVLNGSTNGKMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 325
QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
Db 326 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNERPNGGTISAPGTAKNAI 385
QY 181 TVGATENLRPSFGSVADNINHVAQFSRGPTKDGRIKPDVMAPGTIFLSARSLAPDSF 240
Db 386 TVGATENLRPSFGSVADNINHVAQFSRGPTKDGRIKPDVMAPGTIFLSARSLAPDSF 445
```

```
QY 241 WANHDSKYAYMGCGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
DB 446 WANHDSKYAYMGCGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 505
QY 301 PNGNQGWGRVTLDKSLNVAIVYNESSLSSTSQKATYFTATAGKPLKISLWSDAPASTTA 360
DB 506 PNGNQGWGRVTLDKSLNVAIVYNESSLSSTSQKATYFTATAGKPLKISLWSDAPASTTA 565
QY 361 SVTLVNDLVLITAPNGTOYVGNDFTPSYNDWNWGRNNVFNFINAPOSQGTYYTIEVOAYN 420
DB 566 SVTLVNDLVLITAPNGTRYVGNDFPAPNDWNWGRNNVFNFINAPOSQGTYYTIEVOAYN 625
QY 421 VPVGPQTFSIAIYN 434
DB 626 VPVGPQNFSLAIYN 639

RESULT 4
Q9AQR0_9BACI
ID Q9AQR0_9BACI PRELIMINARY; PRT; 434 AA.
AC Q9AQR0;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Protease (Fragment).
GN Name=PROG;
OS Bacillus sp. NV1.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=133781;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NV1.
RX MEDLINE=20568675; PubMed=11118284; DOI=10.1006/bbrc.2000.3931;
RA Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
RA Horikoshi K.;
RT "Novel oxidatively stable subtilisin-like serine proteases from
RT alkaliphilic Bacillus spp.: enzymatic properties, sequences, and
RT evolutionary relationships.";
RL Biochem. Biophys. Res. Commun. 279:313-319(2000).
DR EMBL; AB046406; BAB21269.1; -; Genomic_DNA.
DR HSSP; P00782; 1SUP.
DR SMR; Q9AQR0; 1-434.
DR MEROPS; S08.123; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept Bact C.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF04151; PPC; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
FT NON_TER 1 1
FT NON_TER 434 434
SQ SEQUENCE 434 AA; 45294 MW; 83517EDDB74125D2 CRC64;

Query Match 95.0%; Score 2138; DB 2; Length 434;
Best Local Similarity 93.3%; Pred. No. 1.2e-131;
Matches 405; Conservative 19; Mismatches 10; Indels 0; Gaps 0;

QY 1 NDVARGIKVADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAPRGKITAYALGRN 60
DB 1 NDVARGIKVADVAQSSYGLYGQGVAVADTGLDTRNDSSMHEAPRGKITAYALGRN 60
QY 61 NANTNGHGHVAGSVLGNSTNKGMAPOANLVFQSIMDSSGGLGGLPSNLTLFSQAYS 120
DB 61 NANTNGHGHVAGSVLGNSTNKGMAPOANLVFQSIMDSSGGLGGLPSNVTLFSQAYS 120
QY 121 AGARIHTNSGAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
DB 121 AGARIHTNSGAPVNGAYTTDSRNVDYVRKNDMAVLFAAGNEGPNNGGTISAPGTAKNAI 180
```

```
QY 181 TVGATENLRPSFGSVADNINHVAQFSSRGPTKGRIKPDVMAPGTFILSARSLAPDSSF 240
DB 181 TVGATENLRPSFGSVADNINHVAQFSSRGPTKGRIKPDVMAPGTFILSARSLAPDSSF 240
QY 241 WANHDSKYAYMGCGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
DB 241 WANHDSKYAYMGCGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
QY 301 PNGNQGWGRVTLDKSLNVAIVYNESSLSSTSQKATYFTATAGKPLKISLWSDAPASTTA 360
DB 301 PNGNQGWGRVTLDKSLNVAIVYNESSLSSTSQKATYFTATAGKPLKISLWSDAPASTTA 360
QY 361 SVTLVNDLVLITAPNGTOYVGNDFTPSYNDWNWGRNNVFNFINAPOSQGTYYTIEVOAYN 420
DB 361 SVTLVNDLVLITAPNGTKYVGNDFTPAYDNNWGRNNVFNFINAPOSQGTYYTIEVOAYN 420
QY 421 VPVGPQTFSIAIYN 434
DB 421 VPQGPQAFSLAIYN 434

RESULT 5
Q9AQR1_9BACI
ID Q9AQR1_9BACI PRELIMINARY; PRT; 433 AA.
AC Q9AQR1;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Protease (Fragment).
GN Name=PROD;
OS Bacillus sp. SD521.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=133780;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SD521;
RX MEDLINE=20568675; PubMed=11118284; DOI=10.1006/bbrc.2000.3931;
RA Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
RA Horikoshi K.;
RT "Novel oxidatively stable subtilisin-like serine proteases from
RT alkaliphilic Bacillus spp.: enzymatic properties, sequences, and
RT evolutionary relationships.";
RL Biochem. Biophys. Res. Commun. 279:313-319(2000).
DR EMBL; AB046405; BAB21268.1; -; Genomic_DNA.
DR HSSP; Q45670; 1DBI.
DR SMR; Q9AQR1; 1-433.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_Bact_C.
DR InterPro; IPR00209; Pept_S8_S53.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF04151; PPC; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
FT NON_TER 1 1
FT NON_TER 433 433
SQ SEQUENCE 433 AA; 45576 MW; 98A2DF18F5660DDC CRC64;

Query Match 88.8%; Score 1998.5; DB 2; Length 433;
Best Local Similarity 87.8%; Pred. No. 1.6e-122;
Matches 381; Conservative 28; Mismatches 24; Indels 1; Gaps 1;

QY 1 NDVARGIKVADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAPRGKITAYALGRN 60
DB 1 NDVARGIKVADVAQSNYGLYGQGVAVADTGLDTRNDSSMHEAPRGKITAYALGRN 60
QY 61 NANTNGHGHVAGSVLGNSTNKGMAPOANLVFQSIMDSSGGLGGLPSNLTLFSQAYS 120
DB 61 NANTNGHGHVAGSVLGN-ALNKGMAPOANLVFQSIMDSSGGLGGLPSNLTLFSQAWN 119
```



```
QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
DB 120 AGARIHTNSWGAANGVAYTTANSRQVDEYVRNNDMTVLFAAGNEGNSGTISAPGTAKNAI 179
QY 181 TVGATENLRPSFGSVADNINHVAFSSRGPTKDGRIKPDVMAAGTFFILSARSLAPDSSF 240
DB 180 TVGATENLRPSFGSLADNPNHIAQFSSRGATRDGRIKPDVTAAGTFFILSARSLAPDSSF 239
QY 241 WANHSKYAYMGTSMATPIVAGNVAQLREHFVKRGITPKPSLKAALIAGAADIGLGY 300
DB 240 WANYSKYAYMGTSMATPIVAGNVAQLREHFVKRGITPKPSLKAALIAGATDVGLGY 299
QY 301 PNGNGGWRVTLDKSLNVAYNNESSLSQKATYSFATAGKPKIKISLVWSDAPASTTA 360
DB 300 PSGDQGWGRVTLDKSLNVAYNNEATALTGQKATYSFQAGKPKIKISLVWTDAPGSTTA 359
QY 361 SYTLVNDLVLITAPNGTQYVGNDFSTPYDNNWDGRNNVFNAPQSGTGTIEVQAYN 420
DB 360 SYTLVNDLVLITAPNGQYVGNDFSPYDNNWDGRNNVFNAPQSGTGTIEVQAYN 419
QY 421 VPVGPQTFSLAIVN 434
DB 420 VPSGQRFSLAIVH 433
RESULT 6
Q9AQR4_9BACI
ID Q9AQR4_9BACI PRELIMINARY; PRT; 433 AA.
AC Q9AQR4;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Protease (Fragment).
GN Name=PROA;
OS Bacillus sp. D6.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=127889;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=D6;
RX MEDLINE=20568675; PubMed=11118284; DOI=10.1006/bbrc.2000.3931;
RA Saeiki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
RA Horikoshi K.;
RT "Novel oxidatively stable subtilisin-like serine proteases from
RT alkaliphilic Bacillus spp.: enzymatic properties, sequences, and
RT evolutionary relationships.";
RL Biochem. Biophys. Res. Commun. 279:313-319 (2000).
DR EMBL; AB046402; BAB21265.1; -; Genomic_DNA.
DR HSSP; Q45670; 1DBI.
DR SMR; Q9AQR4; 1-433.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_Bact_C.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF04151; PPC; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
FT NON_TER 1
FT NON_TER 433
SQ SEQUENCE 433 AA; 45636 MW; 52087EOA2516107F CRC64;
Query Match 88.6%; Score 1994.5; DB 2; Length 433;
Best Local Similarity 87.6%; Pred. No. 2.9e-122;
Matches 360; Conservative 28; Mismatches 25; Indels 1; Gaps 1;
```

```
QY 1 NDVARGIVKADVAQHSYGLYGQCIIVAVADTGLDGRNDSMHFAFRGKITALYALGRTN 60
DB 1 NDVARGIVKADVAQNNYGLYGQGVAVADTGLDGRNDSMHFAFRGKITALYALGRTN 60
```

```
QY 61 NANDTNHGHTHVAGSVLGNSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDPNHGHTHVAGSVLGN-ALNKGMAPQANLVFQSIMDSGGGLGGLPSNLTLFSQAWN 119
QY 121 AGARIHTNSWGAANGVAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
DB 120 AGARIHTNSWGAANGVAYTTANSRQVDEYVRNNDMTVLFAAGNEGNSGTISAPGTAKNAI 179
QY 181 TVGATENLRPSFGSVADNINHVAFSSRGPTKDGRIKPDVMAAGTFFILSARSLAPDSSF 240
DB 180 TVGATENLRPSFGSLADNPNHIAQFSSRGATRDGRIKPDVTAAGTFFILSARSLAPDSSF 239
QY 241 WANHSKYAYMGTSMATPIVAGNVAQLREHFVKRGITPKPSLKAALIAGAADIGLGY 300
DB 240 WANYSKYAYMGTSMATPIVAGNVAQLREHFVKRGITPKPSLKAALIAGATDVGLGY 299
QY 301 PNGNGGWRVTLDKSLNVAYNNESSLSQKATYSFATAGKPKIKISLVWSDAPASTTA 360
DB 300 PSGDQGWGRVTLDKSLNVAYNNEATALTGQKATYSFQAGKPKIKISLVWTDAPGSTTA 359
QY 361 SYTLVNDLVLITAPNGTQYVGNDFSTPYDNNWDGRNNVFNAPQSGTGTIEVQAYN 420
DB 360 SYTLVNDLVLITAPNGQYVGNDFSPYDNNWDGRNNVFNAPQSGTGTIEVQAYN 419
QY 421 VPVGPQTFSLAIVN 434
DB 420 VPSGQRFSLAIVH 433
RESULT 7
Q9AQR2_9BACI
ID Q9AQR2_9BACI PRELIMINARY; PRT; 433 AA.
AC Q9AQR2;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Protease (Fragment).
GN Name=PROC;
OS Bacillus sp. Y.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=133779;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkely;
RX MEDLINE=20568675; PubMed=11118284; DOI=10.1006/bbrc.2000.3931;
RA Saeiki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
RA Horikoshi K.;
RT "Novel oxidatively stable subtilisin-like serine proteases from
RT alkaliphilic Bacillus spp.: enzymatic properties, sequences, and
RT evolutionary relationships.";
RL Biochem. Biophys. Res. Commun. 279:313-319 (2000).
DR EMBL; AB046404; BAB21267.1; -; Genomic_DNA.
DR HSSP; Q45670; 1DBI.
DR SMR; Q9AQR2; 1-433.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_Bact_C.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF04151; PPC; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
FT NON_TER 1
FT NON_TER 433
SQ SEQUENCE 433 AA; 45588 MW; B81291A803C775AE CRC64;
Query Match 88.3%; Score 1987.5; DB 2; Length 433;
Best Local Similarity 87.3%; Pred. No. 8.2e-122;
Matches 379; Conservative 29; Mismatches 25; Indels 1; Gaps 1;
```



```
QY 1 NDVARGIVKADVAHQSYGLYGQGOIVAVADTGLDTRNDSSMHEAFRGKITIYALGRTN 60
DB 1 NDVARGIVKADVAHQSYGLYGQGOIVAVADTGLDTRNDSSMHEAFRGKITIYALGRTN 60
QY 61 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSIMDSGGLGGLPSNLQTLFSQAYS 120
DB 61 NASDPNGHGHVAGSVLGN-ALNKGMAPOANLVFQSIMDSGGLGGLPSNLQTLFSQAWN 119
QY 121 AGARIHTNSWGAANGAYTTDSNRVDDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
DB 120 AGARIHTNSWGAANGAYTANSRQVDEYVRNNDMTVLFPAAGNEGNGGTISAPGTAKNAI 179
QY 181 TVGATENLRPSGVSADNHNHVAOFSRRGPTKGRIPKDPVMAPGTFILSARSLAPDSF 240
DB 180 TVGATENLRPSGVSADNHNHVAOFSRRGATDGRIPKDPVMAPGTFILSARSLAPDSF 239
QY 241 WANHDSKVAYMGTSMTATPAGNVAQRLREHFVNRGIPKPSLLKAALIAAGADIGLY 300
DB 240 WANYNSKVAYMGTSMTATPAGNVAQRLREHFVNRGIPKPSLLKAALIAAGADIGLY 299
QY 301 PNGNOGWRVTLKSLNVAYNSSLSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
DB 300 PNGDGQGWGRVTLKSLNVAYNSSLSQKATYSFTATAGKPLKISLVWSDAPASTTA 359
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTSFVNDWNGRNNVFNAPQSGTITIEVQAYN 420
DB 360 SVTLVNDLVLITAPNGQYVGNDFTSFVNDWNGRNNVFNAPQSGTITIEVQAYN 419
QY 421 VPGPQTESLAIVN 434
DB 420 VPSGQRFSLAIVH 433

RESULT 8
QANB18_9M1CC
ID QANB18_9M1CC PRELIMINARY; PRT; 697 AA.
AC QANB18;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DE Peptidase S8 and S53, subtilisin, kexin, sedolisin.
GN ORFName=ArthDRAFT_0589;
OS Arthrobacter sp. FB24.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcineae; Micrococcaceae; Arthrobacter.
OX NCBI_TaxID=290399;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FB24;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Arthrobacter sp. FB24."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FB24;
RG US DOE Joint Genome Institute (PGP-ORN);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Arthrobacter sp. FB24."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHQ1000025; EAL94539.1; -; Genomic_DNA.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 697 AA; 73821 MW; B8924966C67C0714 CRC64;
```

```
Query Match 38.7%; Score 870.5; DB 2; Length 697;
Best Local Similarity 41.4%; Pred. No. 1.8e-48; Indels 85; Gaps 14;
Matches 209; Conservative 73; Mismatches 138;

QY 1 NDVARGIVKADVAHQSYGLYGQGOIVAVADTGLDTRNDSSMHEAFRGKITIYALGRTN 59
DB 196 NNVAEILNADVQLNGTYYRGAGEVAVADTGFDTG-DAANPHPAFTGRVQTYALGRTA 254
QY 60 -NNANDTNGHGHVAGSVLGNSTN-----KGMAPQANLVFQSIMDSGGLGGLPSNLQ 112
DB 255 PDKADDPHGHGHVAGSVLGRNSATMGAIESTAPEALLILQSLDPPNGGLGGIPVNLN 314
QY 113 TLFSAQYSAGARIHTNSWGA-AVNGAYTTDSNRVDDYVRKN-DMTILFAAGNEGNG-- 167
DB 315 DLFQKTYDDGARKVHTNSWVGPNLIPYDASSREIDFVWNHPDQVICFAAGNDGVDGSD 374
QY 168 -----GTISAPGTAKNAITVGATENLR-----PSFGSY-----ADNHNVA 203
DB 375 GTVDSNLSIGSQAANKCITVGASESLRKEFTSYTYMPGDFPANPVKDKQANNPDGMV 434
QY 204 QFSRRGPTKGRIPKDPVMAPGTFILSARSLAP-DSSFWANHDSKVAYMGTSMATPIVA 262
DB 435 AFSSRGPTKGRIPKDPVMAPGTILSLRNAPMGNTFGTSTDPDLPFFDSGTSMATPLVA 494
QY 263 GNVAQRLREHFVNRGIPKPSLLKAALIAAGADIGLY-----PNGNOGWRVTLK 314
DB 495 GCAAVLRETLVKNGLNPSAALVKALLVNGADVLPQYNPSEAGSPNGSGWGRVNLAR 554
QY 315 SLNV-----AVNNESSLSQKATYSF-----TATAGKP 344
DB 555 SVLPQGNAGLGGEGLEQOQEDSFIDPEEPKVAAGRRNRGPAEALTAAGVT 614
QY 345 LKISLVSDAPASTTASVTLVNDLVLITAPNGTQYVGNDFTSFVNDWNGRNNVFN 404
DB 615 LKITLVMSDPPGP-----QLQNDLVLITADGSRHSGNSTTA---GPDNRNNVEQVLW 666
QY 405 NAPSQGTITIEVQAYNVPVGPQTF 429
DB 667 TGMPPGQARIVVRAFRITQFPQPYA 691

RESULT 9
Q6MKR4_BDEBA
ID Q6MKR4_BDEBA PRELIMINARY; PRT; 711 AA.
AC Q6MKR4;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Subtilisin-like serine protease precursor.
GN Ordered locus names=Bd2321;
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164; DOI=10.1126/science.1093027;
RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
RA Sockett R.B., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
RT genomic perspective."
RL Science 303:689-692(2004).
DR EMBL; EX842652; CAE80143.1; -; Genomic_DNA.
DR HSP; F27693; IAH2.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
```

DR PROSITE; PS00138; SUBTILASE SER; 1.
KW Complete proteome; Protease; Signal.
FT SIGNAL 1 8
SQ SEQUENCE 711 AA; 74914 MW; 4930050843357EE5 CRC64;
Query Match 33.6%; Score 755.5; DB 2; Length 711;
Best Local Similarity 37.7%; Pred. No. 6.2e-41;
Matches 181; Conservative 78; Mismatches 148; Indels 73; Gaps 13;
QY 13 AQHSYGLYGQGIIVAVADTGLTGRNDSMHEAFRGKITALYALGRITNA-NDTNGHGH 71
DB 238 AAWAMGYAGKGTQVSMADTGLDSG-NTGAIHQDFAGGIVISYPPFGLWSKSDPDMGHGH 296
QY 72 VAGSVLNGSTNKGW----APQANLVFOSIMDSGGGLGGLPSNLQTLFSQAYSAGARHT 127
DB 297 VAGSVNGRGTSKGLLKGAYEANNVAGSMSPMKNLSVPSKGLDLFEKAFADGARLHT 356
QY 128 NSWGAA-VNGAYTTDSRVNDYVRKN-DMTILFAAGNEGP-----NGGTISAPGTAK 177
DB 357 NSWGGARTFGAYDNFAVQVDENSYANPDMILILFAAGNSGADKNKGRIDSNMSASPGTAK 416
QY 178 NAITVGATENL-----RPSFGSY-ADNINHVAQFSRRGPTKDG 214
DB 417 NVLTVGASENVTKSGGIQVPIISKRAAKDEWPESEPIYSYISDNGNGLAMFSSRGPTTDDG 476
QY 215 RIKPDVMAPGTFLSARSLAPDSSFWANHDSKYAYMGTSMATPIVAGNVAQLREHFVK 274
DB 477 RTKPDIVAPGNVLSVFSQEKDASPLMGAYNKDYVWSGTSMATPLAAGAAIAIAQVLVE 536
QY 275 NRGI-TPKPSLLKAALIAAGADIGLY-----PNGNGWGRVTLDKSLN 317
DB 537 KLGKMPNSAALMKATMLHTAVDMYFGQFGEIGAARGQELITRRPNSDESGYRVDVANIAN 596
QY 318 VA-----YNNSSSLTSOKATYSFTATAGPKLKI SLWSDAPASTTASVTLVNDLDLVIT 373
DB 597 LGGATQFVDNRQGVAGAEVSYEFTLNAPGSLYANLVNTDAPGSANAQAALVNDLDLVIT 656
QY 374 APNGTQYVGNDFTSYNDNDWGRNVENVFNAPQSGTYTTEVQAYNVPV---GQPTFSL 430
DB 657 LPNGQTLSNNDHI-----NNLEMKSLGSPAGTYKLVTKGFKVPGQKNGQAAYAL 706
RESULT 10
Q4HUV5_9DELT PRELIMINARY; PRT; 1748 AA.
AC Q4HUV5;
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Peptidase S8 and S53, subtilisin, kexin, sedolisin, Nepovirus coat protein, N-terminal; Nepovirus coat protein, N-terminal precursor.
GN ORFNames=AdehDRAFT_3007;
OS Anaeromyxobacter dehalogenans 2CP-C.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
OX NCBI_TaxID=290397;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Ptluck S., Richardson P.,
RT "Sequencing of the draft genome assembly of Anaeromyxobacter dehalogenans 2CP-C."
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Anaeromyxobacter dehalogenans 2CP-C."
RL Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
CC EMBL; AH001000011; EAL79523.1; -; Genomic_DNA.
DR Capelid protein; Signal.
KW SIGNAL 1 23
SQ SEQUENCE 1748 AA; 177411 MW; B1EGDE33BE81DE76 CRC64;
Query Match 32.6%; Score 734.5; DB 2; Length 1748;
Best Local Similarity 39.9%; Pred. No. 4.8e-39;
Matches 191; Conservative 66; Mismatches 155; Indels 67; Gaps 19;
QY 1 NDVARGIVK----ADVAQHSYGLYGQGIIVAVADTGLD-----TGRNDSMHEAFR 47
DB 248 NDTSRWTITQYTPSDTSISDRGLDGRGQIVAGTGLDHDACWFRDPTGAAAGPMHR--- 304
QY 48 KQITALYALGRITNANDTN-GHGTAVAGSVLGN-----GSTNKGMAQANLVFOSIMDS 100
DB 305 -KVAAYLTVG--GDDYDGNLGHGTAVAGTQDQPTTGGAAANGMAPGARVVVVDLFLG 361
QY 101 GGLGLGPSNLQTLFSQAYSAGARHTNSWGAAVNGAYTTDSRVNDYVRKN-DMTILFA 159
DB 362 ENNWFPPADLAELFTTPYALGARHTNSWSSN-AVDALARSADRWFHWPDLVLFA 420
QY 160 AGNEGPNGGTISAPGTAKNAITVGATENLRFSFGSYADNINHVAQFSRGPTKDGRIKPD 219
DB 421 NGNAGPDVGVGAPATAKNVSVGATG-----GLAED---VASFSSHGPAADGRTKPT 472
QY 220 VMAPGTFTLSARSLAPDSSFWANHDSKYAYMGTSMATPIVAGNVAQLREHFVK---R 276
DB 473 LTPAGVGIVSADSDGTPAS---NNCSTVAF-SGTSMATPAAAGAAALVRQYFEGGFWPS 527
QY 277 GI-----TPKPSLLKAALIAAGADI-----GLG-YPNGNGWGRVTLDKSLNVA----- 319
DB 528 GLGSPADRSAAALVKAATLVNSAQNVAGENGNGPIPTGQGWGRINLSNARLPADRAY 587
QY 320 --YNNSSSLTSOKATYSFTATAGPKLKI SLWSDAPASTTASVTLVNDLDLVITAPNG 377
DB 588 LDVVEVAAGLETGSGFTQVFTGAPQLKLTIVNTDAPGSLADRSVNDLDLVITVPGG 647
QY 378 -TQYVGNDFTSYNDNDWGRNVENVFNAPQSGTYTTEVQAYNVPVPGQPTFSLAI 432
DB 648 ATTVLGNVFALGESVAGAPDLNVEEQVLLAAPTVGTYTVRVTGYNVPGVPGQPFALVI 706
RESULT 11
Q4HUV5_GIBZE PRELIMINARY; PRT; 1088 AA.
AC Q4HUV5;
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=FG11223.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocrematiaceae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=229533;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S., Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L., Boukhaltier B., Butler J., Calvo S.E., Camarata J., Chang J., Diaz J.S., Dooley K., Cooke P., Corum B., Dearellano K., Erickson J., Farro S., Ferreira P., Fitzgerald M., Gage D., Galagan J., Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N., Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I., Jaffe D., Johnson R., Jones C., Kamal M., Katat A., Karatas A., Kellis C., Landers T., Levine R., Lindblad-Toh K., Liu G., Liu A., Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J., Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,

13-SEP-2005 (TRENBLREL. 31, Last annotation update)
DE ABC transporter B family protein.
GN Name=tagC; ORFNames=DD0191192;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxId=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Turgall A.F., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey F.,
RA Bankier A., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhrou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Loulsegod H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAFI01000133; EAL64353.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR011527; ABC membrane 1.
DR InterPro; IPR001140; ABC TM transp.
DR InterPro; IPR003439; ABC transp like.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF00864; ABC membrane_1.
DR Pfam; PF00005; ABC tran; 1.
DR Pfam; PF00082; Peptidase S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR ProDom; PD000006; ABC transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00929; ABC TM1F; 1.
DR PROSITE; PS00211; ABC TRANSPORTER 1; 1.
DR PROSITE; PS00893; ABC TRANSPORTER 2; 1.
DR PROSITE; PS00137; SUBTILASE HIS; 1.
SQ SEQUENCE 1741 AA; 193884 MW; 44DEC61D68E4947D CRC64;
Query Match 23.6%; Score 531.5; DB 2; Length 1741;
Best Local Similarity 28.1%; Pred. No. 9.1e-26;
Matches 166; Conservative 81; Mismatches 149; Indels 195; Gaps 24;
QY 19 LYGGQGVAVATGDTGTR---NDS-----SMHEAFRGKITALYALGRNTNANDTNGH 68
DB 314 LRKGQGLISADTGLDGSCHFFSDSKYPIPLNSVNLNR-KVVTYITTSDDSKVDGH 372
QY 69 GTHVAGSVLGL-----NGSTNRKGMAPQANLVFQSIMDSGGGLGL--PSNLQTLFSQAY 119
DB 373 GTHICGSAAGTPEDSSVNISSFSGLATDAKIAF---FDLASGSSSLTPPSDLKQLYQPLY 429
QY 120 SAGARIHTNSWGA-----AVNGAYTTDSRNVDDYVRKN-DMTILPAAAGNPGNGGTIS--A 172
DB 430 DAGARVHCDSWGSVSVEGTGYSSTASIDDFLTHPDFFILRAAGN---NEQYLSLIT 486

173 PGTAKNAITVGATENLR-----PSFGSYADNI----- 199
DB 487 QSTAKNIVTGAHQTHIENYLTGDPNYINYOSSVDINQELICDFDSRYCNYNTTAQCCLLES 546
QY 200 -----NHVAQFSRGPTKDGRIKPDVMAQGTFTIL 228
DB 547 NATTGLASCCPTLLRKSVIDAANTOPLYNNENCSFSGKGTGDRMKPDLVAFGEYIT 606
QY 229 SARSSLA-----PDSSFWAHDHDKYAYMGGTSMATPIVAGNVAAQLREH-----F 272
DB 607 SARSGANTTCQCGDSL-PNINALLA-IGSTSMATSPAAATATILROYLVGDYVYPTGSI 664
QY 273 VNRGITPKPSLLKAAITAGA-----ADIGLGPNGV-----QGWGRVT 311
DB 665 VESNKLQPTGSLKALMINNAQLLNGTFLQTLITSSITYPNSQVFNFAFASLVQGWGAIR 724
QY 312 LDKSLNAVYVNESS-----SLTSOKATYSFT-- 338
DB 725 MSNHLVHVNNNNNNNNNTSGITKVFVIGGLDLRLVKNQWKEESLSTGQNTSYCFYTK 784
QY 339 -----ATAGKPLK---ISLVMSDAPASTTASVTLVNDLGLV-----TAPNGT 378
DB 785 PSSSSSSGNNIPRVVATLVWTDPPSYAGAKFNLVNLDLTMIYYRDNGSTIFYSNQGS 844
QY 379 QYVGNDFTSPYNDWGRNNVFNAPQSGTYTIEVOAYNVPGPQTFS 429
DB 845 SPLG---LAPTQDT---LNNVEGIVHNPTETPTMVFVAGTVNPMGPQNFS 889

RESULT 14
TAGC_DICDI
ID TAGC_DICDI STANDARD; PRT; 1743 AA.
AC Q23868;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Prestalk-specific protein tagC precursor (EC 3.4.21.-).
GN Name=tagC;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxId=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX MEDLINE=97140317; PubMed=8986798; DOI=10.1073/pnas.93.26.15260;
RA Shauleky G., Escalante R., Loomis W.F.;
RT "Developmental signal transduction pathways uncovered by genetic
suppressors.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:15260-15265(1996).
CC -!- FUNCTION: Intercellular communication via tagC may mediate
integration of cellular differentiation with morphogenesis (By
similarity).
CC -!- SIMILARITY: Contains 1 ABC transmembrane type-1 domain.
CC -!- SIMILARITY: Contains 1 ABC transporter domain.
CC -!- SIMILARITY: Contains 1 peptidase S8 domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC EMBL; U60086; AAB03331.1; -; mRNA.
DR PIR; T18279; T18279.
DR HSP; P08716; LMT0.
DR DictyBase; DDB0001795; tagC.
DR InterPro; IPR011527; ABC membrane 1.
DR InterPro; IPR001140; ABC TM transp.
DR InterPro; IPR003439; ABC transp like.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF00864; ABC membrane_1.
DR Pfam; PF00005; ABC tran; 1.

DR Pfam: PF00082; Peptidase S8; 1.
 DR PRINTS; PR00723; SUBTILISIN.
 DR ProDom; PD000006; ABC_TRANSPORTER; 1.
 DR PROSITE; PS00929; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
 DR PROSITE; PS00136; SUBTILASE ASP; FALSE_NEG.
 DR PROSITE; PS00137; SUBTILASE_HIS; 1.
 DR PROSITE; PS00138; SUBTILASE_SER; FALSE_NEG.
 DR ATP-binding; Glycoprotein; Hydrolase; Nucleotide-binding; Protease;
 KW Serine protease; Signal; Transmembrane; Transport.
 FT SIGNAL 1 27 Potential.
 FT CHAIN 28 1743 Prestalk-specific protein tagC.
 FT TRANSMEM 962 982 Potential.
 FT TRANSMEM 1027 1047 Potential.
 FT TRANSMEM 1072 1092 Potential.
 FT TRANSMEM 1157 1177 Potential.
 FT TRANSMEM 1260 1280 Potential.
 FT TRANSMEM 1288 1308 Potential.
 FT DOMAIN 1031 1314 ABC transmembrane type-1.
 FT DOMAIN 1450 1687 ABC transporter.
 FT NP_BIND 1485 1492 ATP (Potential).
 FT REGION 316 642 Serine protease.
 FT COMBIAS 42 46 Poly-Aen.
 FT COMBIAS 94 103 Poly-Aen.
 FT COMBIAS 643 646 Poly-Ala.
 FT COMBIAS 733 741 Poly-Aen.
 FT COMBIAS 786 792 Poly-Ser.
 FT COMBIAS 1337 1340 Poly-Glu.
 FT COMBIAS 1346 1352 Poly-Gly.
 FT COMBIAS 1353 1357 Poly-Aen.
 FT COMBIAS 1358 1364 Poly-Aen.
 FT COMBIAS 1381 1386 Poly-Aen.
 FT COMBIAS 1707 1729 Poly-Aen.
 FT ACT_SITE 325 325 Charge relay system (By similarity).
 FT ACT_SITE 372 372 Charge relay system (By similarity).
 FT ACT_SITE 637 637 Charge relay system (By similarity).
 FT CARBOHYD 390 390 N-linked (GlcNAc..). (Potential).
 FT CARBOHYD 536 536 N-linked (GlcNAc..). (Potential).
 FT CARBOHYD 547 547 N-linked (GlcNAc..). (Potential).
 FT CARBOHYD 614 614 N-linked (GlcNAc..). (Potential).
 FT CARBOHYD 689 689 N-linked (GlcNAc..). (Potential).
 FT CARBOHYD 735 735 N-linked (GlcNAc..). (Potential).
 FT CARBOHYD 741 741 N-linked (GlcNAc..). (Potential).
 FT CARBOHYD 776 776 N-linked (GlcNAc..). (Potential).
 FT CARBOHYD 832 832 N-linked (GlcNAc..). (Potential).
 FT CARBOHYD 887 887 N-linked (GlcNAc..). (Potential).
 FT CARBOHYD 1251 1251 N-linked (GlcNAc..). (Potential).
 FT CARBOHYD 1385 1385 N-linked (GlcNAc..). (Potential).
 FT CARBOHYD 1386 1386 N-linked (GlcNAc..). (Potential).
 FT CARBOHYD 1454 1454 N-linked (GlcNAc..). (Potential).
 FT CARBOHYD 1704 1704 N-linked (GlcNAc..). (Potential).
 SQ SEQUENCE 1743 AA; 194146 MW; 12DB363E2F729839 CRC64;
 Query Match 23.3%; Score 523.5; DB 1; Length 1743;
 Best Local Similarity 27.9%; Pred. No. 3.1e-25;
 Matches 165; Conservative 81; Mismatches 150; Indels 195; Gaps 24;
 QY 19 LYQGQGIIVADTGLDTGR---NDS-----SMHEAFRGKITALVALGRNTNANDTNGH 68
 DB 314 LRKGQILSIADTGLDGSCHFFDSKYPIPLNSVNLNR-KVVTYTTTSDSDKVDGH 372
 QY 69 GTHVAGSVLGL-----NGSTKNGMAPQANLVFQSTMDSGGGGLGHL--PSNLQTLFSQAY 119
 DB 373 GTHICSAAGTPEDSSVNISSFGLATDAKIAF---FDLASGSSSITPPSLDKQLYQPLY 429
 QY 120 SAGARITHNSWGA-----AVNGATYTSRNVDDIVRNK-DWTLFPAAGNPGNGGTIS--A 172
 DB 430 DAGARVHCDWSGVSVEGYTGSYSSTASIDDFLTHPDFFILRAAGN---NEQYLSLET 486
 QY 173 PGTAKNAITVGATENLR-----PSFGSYADNI----- 199
 DB 487 QSTAKNVITVGAHQTHENYLTGPNYINYSQSSVDINQBELICDFDSRYCNYYTAQCCLRS 546

QY 200 -----NHVAQFSSRGPTKDGRIKPDVMAQCTFIL 228
 DB 547 NATTGLASCCPTLLRRKSVIDAANTOPLLYNNENNICSFSSKGPHTDGRMKPALVAPGEYIT 606
 QY 229 SARSSILA-----PDSSFWANHDSKYAYMGGSMTATPIVAGNVAQREH-----F 272
 DB 607 SARSGNANTDQCGDGLS-PNTNALLA-ISGISMATSFAAATATILRLQVLVDGYPTGSI 664
 QY 273 VKNRGITPKPSLLKAALIAGA-----ADIGLYPNGN-----QGWGRVT 311
 DB 665 VESNKLQPTGSLLKALMINNAQLNGTFLQITSSSITYPSNOVFENFAGASLVQGWGAIR 724
 QY 312 LKSLNVAIVNESS-----SLSTSOKATYSFT-- 338
 DB 725 MSNWLHVNNNNNNNNNNKTSDGITKPDGIGLDRLVKPNQWKESLSTGQNTSYCFTYK 784
 QY 339 -----ATACKPLK---ISLVWSDAPASTTASVTLVNDLQV-----TAPNGT 378
 DB 785 PSSSSNSGNIPRVVATILVTDPSYAGAKFNVLNNLDLTMIIYRDNGSTIFYSNQGS 844
 QY 379 QYVGNDFTPSYNDNMDGRNVNFINAPQSGTYTIEVOAYNVVGPQTF 429
 DB 845 SFLG---LAPTQDT---LNNVEGIVHNPTPEMTYREVMWAGTNVPMGPQNF 889
 RESULT 15
 Q8T9W1.DICDI PRELIMINARY; PRT; 1825 AA.
 AC Q8T9W1;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Serine protease/ABC transporter TagD (ABC transporter B family protein).
 GN Name:tagD; ORFNames=DD80191427;
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AX4;
 RA Anjard C., Loomis W.F.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AX4;
 RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
 RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
 RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
 RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
 RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
 RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
 RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
 RA Cooper J., Haydock S., Van Driessche N., Cronin A., Goodhead I.,
 RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsey R.,
 RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
 RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
 RA Loulaeged H., Mungall K., Oliver K., Price C., Quail M.A.,
 RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
 RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
 RA Sugano S., White B., Walker D., Woodcock G., Rosenthal A., Tanaka Y.,
 RA Shaulsky G., Schleicher M., Weinstein G., Cox E.C.,
 RA Chisholm R.L., Gibbs R., Loomis W.P., Platzler M., Kay R.R.,
 RA Williams J., Dear P.H., Noegel A.A., Bartell B., Kupepa A.;
 RT "The genome of the social amoeba Dictyostelium discoideum.";
 RL Nature 0:0-0(2005).
 DR EMBL; AF466309; AAL74253.1; -; Genomic_DNA.
 DR EMBL; AAF01080133; EAL64354.1; -; Genomic_DNA.
 DR HSSP; P08716; 1MT0.
 DR DickeyBase; DDB0191427; tagD.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 7, 2006, 09:33:49 ; Search time 82 Seconds
(without alignments)
2211.438 Million cell updates/sec

Title: US-10-820-714A-1-HIS15
Perfect score: 2251
Sequence: 1 NDVARGIVKADVAQHSYGLY.....EVQAYNVPVGPQTFSIAIVN 434

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2242	99.6	434	3	US-09-985-689A-1
2	2242	99.6	434	4	US-10-385-662-2
3	2242	99.6	434	4	US-10-456-479-2
4	2242	99.6	434	4	US-10-837-566-1
5	2242	99.6	434	5	US-10-820-712A-1
6	2242	99.6	434	5	US-10-820-714A-1
7	2242	99.6	640	3	US-09-920-954-6
8	2242	99.6	640	4	US-10-456-479-4
9	2242	99.6	640	4	US-10-784-870-6
10	2242	99.6	640	5	US-10-820-712A-3
11	2242	99.6	640	5	US-10-820-714A-3
12	2237	99.4	434	4	US-10-456-479-11
13	2237	99.4	434	5	US-10-820-712A-14
14	2237	99.4	434	5	US-10-820-714A-15
15	2237	99.4	640	3	US-09-920-954-8
16	2237	99.4	640	4	US-10-784-870-8
17	2186	97.1	434	3	US-09-985-689A-2
18	2186	97.1	434	4	US-10-456-479-10
19	2186	97.1	434	4	US-10-837-566-2
20	2186	97.1	434	5	US-10-820-712A-12
21	2186	97.1	434	5	US-10-820-714A-13
22	2178	96.8	639	3	US-09-920-954-4
23	2178	96.8	639	4	US-10-784-870-4
24	2150	95.5	639	3	US-09-920-954-1
25	2150	95.5	639	4	US-10-784-870-1
26	2150	95.5	640	3	US-09-920-954-2
27	2150	95.5	640	4	US-10-784-870-2

28	2138	95.0	434	3	US-09-985-689A-6
29	2138	95.0	434	4	US-10-456-479-15
30	2138	95.0	434	4	US-10-837-566-6
31	2138	95.0	434	5	US-10-820-712A-22
32	2138	95.0	434	5	US-10-820-714A-23
33	2125.5	94.4	433	3	US-09-985-689A-7
34	2125.5	94.4	433	4	US-10-456-479-16
35	2125.5	94.4	433	4	US-10-837-566-7
36	2125.5	94.4	433	5	US-10-820-712A-23
37	2125.5	94.4	433	5	US-10-820-714A-24
38	1998.5	88.8	433	3	US-09-985-689A-5
39	1998.5	88.8	433	4	US-10-456-479-14
40	1998.5	88.8	433	4	US-10-837-566-5
41	1998.5	88.8	433	5	US-10-820-712A-20
42	1998.5	88.8	433	5	US-10-820-714A-21
43	1994.5	88.6	433	3	US-09-985-689A-3
44	1994.5	88.6	433	4	US-10-456-479-12
45	1994.5	88.6	433	4	US-10-837-566-3

ALIGNMENTS

RESULT 1
US-09-985-689A-1
; Sequence 1, Application US/09985689A
; Publication NO. US20030022351A1
; GENERAL INFORMATION:
; APPLICANT: HATADA, YUJI
; APPLICANT: OGAWA, AKINORI
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483USO
; CURRENT APPLICATION NUMBER: US/09/985,689A
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-985-689A-1

Query Match		99.6%	Score 2242;	DB 3;	Length 434;
Best Local Similarity		99.8%	Pred. No. 2e-170;		
Matches 433;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	NDVARGIVKADVAQHSYGLYGGQIVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN 60			
Db	1	NDVARGIVKADVAQSSYGLYGGQIVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN 60			
Qy	61	NANDTNGHTHVAGSVLNGSTNKGMAQANLVFQSIIMDSGGGLGGLPSNLQTLPSQAYS 120			
Db	61	NANDTNGHTHVAGSVLNGSTNKGMAQANLVFQSIIMDSGGGLGGLPSNLQTLPSQAYS 120			
Qy	121	AGARHTNWSGAANVNGATYTTDSRNVDYVRKNDMTILFAAGNEGNGGTTISAPGTAKNAI 180			
Db	121	AGARHTNWSGAANVNGATYTTDSRNVDYVRKNDMTILFAAGNEGNGGTTISAPGTAKNAI 180			
Qy	181	TVGATENLRPSFGSYADNINHVAQFSRGPDKGRIPKPDVMAPGTFFILSARSLAPDSF 240			
Db	181	TVGATENLRPSFGSYADNINHVAQFSRGPDKGRIPKPDVMAPGTFFILSARSLAPDSF 240			
Qy	241	WANHDSKYAYMGTSMTATPIVAGNVAQUREHFVKNRGITPKPSLLKAAIAGAADIGLY 300			

Db 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVNKRGITPKPSLLKAALIAGAADI GLGY 300
QY 301 PNGNGWGRVTLDKSLNAVYVNESSLSSTSQKATYSFTATAGKPKIKISLWSDAPASTTA 360
Db 301 PNGNGWGRVTLDKSLNAVYVNESSLSSTSQKATYSFTATAGKPKIKISLWSDAPASTTA 360
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNWDGRNNVENVFVINAPOS GTTYTIEVQAYN 420
Db 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNWDGRNNVENVFVINAPOS GTTYTIEVQAYN 420
QY 421 VPVGPQTFSLAIVN 434
Db 421 VPVGPQTFSLAIVN 434

RESULT 2

US-10-385-662-2
; Sequence 2, Application US/10385662
; Publication No. US20040002432A1
; GENERAL INFORMATION:
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: SAITO, KAZUHIRO
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: IZAWA, YOSHIFUMI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KOBAYASHI, TOHRU
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: Alkaline protease
; FILE REFERENCE: 234938US0
; CURRENT APPLICATION NUMBER: US/10/385,662
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: JP 2002-081428
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: JP 2002-165987
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: JP 2002-304230
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: JP 2002-304231
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-385-662-2

Query Match 99.6%; Score 2242; DB 4; Length 434;
Best Local Similarity 99.8%; Pred. No. 2e-170;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAQHSYGLYGOGQIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQHSYGLYGOGQIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
Db 121 AGARHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSVADNINHVAQFSRSGPTKDGRIKPDVMAPGTFILSARSLAPDSF 240
Db 181 TVGATENLRPSFGSVADNINHVAQFSRSGPTKDGRIKPDVMAPGTFILSARSLAPDSF 240
QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVNKRGITPKPSLLKAALIAGAADI GLGY 300
Db 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVNKRGITPKPSLLKAALIAGAADI GLGY 300
QY 301 PNGNGWGRVTLDKSLNAVYVNESSLSSTSQKATYSFTATAGKPKIKISLWSDAPASTTA 360
Db 301 PNGNGWGRVTLDKSLNAVYVNESSLSSTSQKATYSFTATAGKPKIKISLWSDAPASTTA 360
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNWDGRNNVENVFVINAPOS GTTYTIEVQAYN 420
Db 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNWDGRNNVENVFVINAPOS GTTYTIEVQAYN 420
QY 421 VPVGPQTFSLAIVN 434

QY 301 PNGNGWGRVTLDKSLNAVYVNESSLSSTSQKATYSFTATAGKPKIKISLWSDAPASTTA 360
Db 301 PNGNGWGRVTLDKSLNAVYVNESSLSSTSQKATYSFTATAGKPKIKISLWSDAPASTTA 360
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNWDGRNNVENVFVINAPOS GTTYTIEVQAYN 420
Db 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNWDGRNNVENVFVINAPOS GTTYTIEVQAYN 420
QY 421 VPVGPQTFSLAIVN 434
Db 421 VPVGPQTFSLAIVN 434
RESULT 3
US-10-456-479-2
; Sequence 2, Application US/10456479
; Publication No. US20040072321A1
; GENERAL INFORMATION:
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: TAKIMURA, YASUSHI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: NOMURA, MASAFUMI
; APPLICANT: KOBAYASHI, TOHRU
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 238700US0
; CURRENT APPLICATION NUMBER: US/10/456,479
; CURRENT FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: JP 2002-186387
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: JP 2002-304232
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-456-479-2

Query Match 99.6%; Score 2242; DB 4; Length 434;
Best Local Similarity 99.8%; Pred. No. 2e-170;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAQHSYGLYGOGQIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQHSYGLYGOGQIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
Db 121 AGARHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSVADNINHVAQFSRSGPTKDGRIKPDVMAPGTFILSARSLAPDSF 240
Db 181 TVGATENLRPSFGSVADNINHVAQFSRSGPTKDGRIKPDVMAPGTFILSARSLAPDSF 240
QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVNKRGITPKPSLLKAALIAGAADI GLGY 300
Db 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVNKRGITPKPSLLKAALIAGAADI GLGY 300
QY 301 PNGNGWGRVTLDKSLNAVYVNESSLSSTSQKATYSFTATAGKPKIKISLWSDAPASTTA 360
Db 301 PNGNGWGRVTLDKSLNAVYVNESSLSSTSQKATYSFTATAGKPKIKISLWSDAPASTTA 360
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNWDGRNNVENVFVINAPOS GTTYTIEVQAYN 420
Db 361 SVTLVNDLVLITAPNGTQYVGNDFTSYNDNWDGRNNVENVFVINAPOS GTTYTIEVQAYN 420
QY 421 VPVGPQTFSLAIVN 434


```
Db 421 VPVGPQTFSLAIVN 434
|||||
RESULT 4
US-10-837-566-1
; Sequence 1, Application US/10837566
; Publication No. US20040203129A1
; GENERAL INFORMATION:
; APPLICANT: HATADA, YUJI
; APPLICANT: OGAWA, AKINORI
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483US0
; CURRENT APPLICATION NUMBER: US/10/837,566
; PRIOR FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: US/09/985,689A
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-837-566-1

Query Match 99.6%; Score 2242; DB 4; Length 434;
Best Local Similarity 99.8%; Pred. No. 2e-170;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNGHGTTHVAGSVLGNSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NANDTNGHGTTHVAGSVLGNSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTTFILSARSSLAPDSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTTFILSARSSLAPDSF 240
QY 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKRGIPTKPSLLKAALIAGNADIGLY 300
Db 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKRGIPTKPSLLKAALIAGNADIGLY 300
QY 301 PNGNQGWGRVTLDKSLNVAYNVNESSLSSTSQATYSFTATAGKPKLSLVWSDAPASTTA 360
Db 301 PNGNQGWGRVTLDKSLNVAYNVNESSLSSTSQATYSFTATAGKPKLSLVWSDAPASTTA 360
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTSFYNDNWDGRNNVENVFINAPQSGTYYTIEVOAYN 420
Db 361 SVTLVNDLVLITAPNGTQYVGNDFTSFYNDNWDGRNNVENVFINAPQSGTYYTIEVOAYN 420
QY 421 VPVGPQTFSLAIVN 434
Db 421 VPVGPQTFSLAIVN 434

RESULT 5
US-10-837-566-1
; Sequence 1, Application US/10837566
; Publication No. US20040203129A1
; GENERAL INFORMATION:
; APPLICANT: HATADA, YUJI
; APPLICANT: OGAWA, AKINORI
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483US0
; CURRENT APPLICATION NUMBER: US/10/837,566
; PRIOR FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: US/09/985,689A
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-837-566-1

Query Match 99.6%; Score 2242; DB 4; Length 434;
Best Local Similarity 99.8%; Pred. No. 2e-170;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNGHGTTHVAGSVLGNSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NANDTNGHGTTHVAGSVLGNSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTTFILSARSSLAPDSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTTFILSARSSLAPDSF 240
QY 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKRGIPTKPSLLKAALIAGNADIGLY 300
Db 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKRGIPTKPSLLKAALIAGNADIGLY 300
QY 301 PNGNQGWGRVTLDKSLNVAYNVNESSLSSTSQATYSFTATAGKPKLSLVWSDAPASTTA 360
Db 301 PNGNQGWGRVTLDKSLNVAYNVNESSLSSTSQATYSFTATAGKPKLSLVWSDAPASTTA 360
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTSFYNDNWDGRNNVENVFINAPQSGTYYTIEVOAYN 420
Db 361 SVTLVNDLVLITAPNGTQYVGNDFTSFYNDNWDGRNNVENVFINAPQSGTYYTIEVOAYN 420
QY 421 VPVGPQTFSLAIVN 434
Db 421 VPVGPQTFSLAIVN 434

RESULT 6
US-10-820-714A-1
; Sequence 1, Application US/10820712A
; Publication No. US20050026804A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuyoshi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Sumitomo, Nobuyuki
; APPLICANT: Takimura, Yasushi
; APPLICANT: Sato, Teu-yoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
US-10-820-712A-1
; Sequence 1, Application US/10820712A
; Publication No. US20050026804A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuyoshi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Sumitomo, Nobuyuki
; APPLICANT: Takimura, Yasushi
; APPLICANT: Sato, Teu-yoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
```

```

; FILE REFERENCE: 251697US0
; CURRENT APPLICATION NUMBER: US/10/820,714A
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 2003-106709
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-820-714A-1

Query Match      99.6%; Score 2242; DB 5; Length 434;
Best Local Similarity 99.8%; Pred. No. 2e-170;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 NDVARGITVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHAEFRGKITALYALGRTN 60
Db      1 NDVARGILVKADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHAEFRGKITALYALGRTN 60

QY      61 NANDTNGHGHTHVAGSVLNGSTNGKMAPOANLVFQSIWDSGGGLGGLPSNLQTLFQSQAYS 120
Db      61 NANDTNGHGHTHVAGSVLNGSTNGKMAPOANLVFQSIWDSGGGLGGLPSNLQTLFQSQAYS 120

QY      121 AGARIHTNSGAAVNGAYTTDSRVNDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db      121 AGARIHTNSGAAVNGAYTTDSRVNDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180

QY      181 TVGATENLRFPSFGSYADNINHVAQFSSRGPTKCGRIKPDVWMAPTGTFILSARSSSLAPDSSF 240
Db      181 TVGATENLRFPSFGSYADNINHVAQFSSRGPTKCGRIKPDVWMAPTGTFILSARSSSLAPDSSF 240

QY      241 WANHDSKYAYMGGTSMATPIVAGNVAQLRHFHVKNRGITPKPSLLKAALIAGAADIGLGY 300
Db      241 WANHDSKYAYMGGTSMATPIVAGNVAQLRHFHVKNRGITPKPSLLKAALIAGAADIGLGY 300

QY      301 PNGNQGWGRVTLDKSLNVAYNNESSLSSTQKATYSFTATAGKPKILSLVWSDAPASTTA 360
Db      301 PNGNQGWGRVTLDKSLNVAYNNESSLSSTQKATYSFTATAGKPKILSLVWSDAPASTTA 360

QY      361 SVTLVNDLDLVITAPNGTQVYGNDFTPYNDNDWGRNNVENVFVINAPOSQGYTTIEVQAYN 420
Db      361 SVTLVNDLDLVITAPNGTQVYGNDFTPYNDNDWGRNNVENVFVINAPOSQGYTTIEVQAYN 420

QY      421 VPVGPOTFSLAIVN 434
Db      421 VPVGPOTFSLAIVN 434

```

RESULT 7
US-09-920-954-6
; Sequence 6, Application US/09920954
; Publication No. US20020064854A1
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUW
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-0PCT
; CURRENT APPLICATION NUMBER: US/09/920,954
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 03/509,814
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JF98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08

```

; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-920-954-6

Query Match          99.6%; Score 2242; DB 3; Length 640;
Best Local Similarity 99.8%; Pred. No. 3.4e-170;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  NDVARGITVKADVAQHSYGLYGQGIIVAVADTGLDTRGNDSSMHEAFRGKITALYALGRTN 60
Db      207 NDVARGITVKADVAQSSYGLYGQGIIVAVADTGLDTRGNDSSMHEAFRGKITALYALGRTN 266

Qy      61  NANTDTGHGTHVAGSVLNGSTNKGMAPAQNLVPQSIMDSGGGLGGILPSNLQTLFSAQYS 120
Db      267 NANTDTGHGTHVAGSVLNGSTNKGMAPAQNLVPQSIMDSGGGLGGILPSNLQTLFSAQYS 326

Qy      121 AGARIHTNSGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db      327 AGARIHTNSGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386

Qy      181 TVGATENLRPFSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPTGTFILSARSSLPADSSF 240
Db      387 TVGATENLRPFSFGSYADNINHVAQFSRSGPTKDGRIKPDVMAPTGTFILSARSSLPADSSF 446

Qy      241 WANHDSKYAYMGGTSMATPIVAGNVAQLRHHFVKVNRGITPKPSLLKAALITAGADIGLY 300
Db      447 WANHDSKYAYMGGTSMATPIVAGNVAQLRHHFVKVNRGITPKPSLLKAALITAGADIGLY 506

Qy      301 PNGNQHGGRVTLDKSLNVAVYNESSLSLTSQKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db      507 PNGNQHGGRVTLDKSLNVAVYNESSLSLTSQKATYSFTATAGKPLKISLVMSDAPASTTA 566

Qy      361 SVTLVNDLDLVITAPNGTQVVGNDFTSPYNDNDMDGRNNVENVFINAPQSGTGYTTIEVQAYN 420
Db      567 SVTLVNDLDLVITAPNGTQVVGNDFTSPYNDNDMDGRNNVENVFINAPQSGTGYTTIEVQAYN 626

Qy      421 VPVGPQTFSIAIYN 434
Db      627 VPVGPQTFSIAIYN 640

```

```

RESULT 8
US-10-456-479-4
; Sequence 4, Application US/10456479
; Publication No. US20040072321A1
; GENERAL INFORMATION:
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: TAKIMURA, YASUSHI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: NOMURA, MASAFUMI
; APPLICANT: KOBAYASHI, TOHRU
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 238700U0
; CURRENT APPLICATION NUMBER: US/10/456,479
; CURRENT FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: JP 2002-186387
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: JP 2002-304232
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-456-479-4

```

Query Match 99.6%; Score 2242; DB 4; Length 640;

Best Local Similarity 99.8%; Pred. No. 3.4e-170; Mismatches 1; Indels 0; Gaps 0;
Matches 433; Conservative 0;

QY 1 NDVARGIVKADVAQSSYGLYGOGQIVAVADTGLDTRNDSSMHEAPRGKITIYALGRTN 60
|||||
DB 207 NDVARGIVKADVAQSSYGLYGOGQIVAVADTGLDTRNDSSMHEAPRGKITIYALGRTN 266
QY 61 NANDTNGHGTTHVAGSVLGNSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
|||||
DB 267 NANDTNGHGTTHVAGSVLGNSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
|||||
DB 267 NANDTNGHGTTHVAGSVLGNSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
|||||
DB 327 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 386
QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGPTFILSARSSLAPDSSF 240
|||||
DB 327 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 386
QY 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNGRGTIPKPSLLKAAALIAGNADIGLGY 300
|||||
DB 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGPTFILSARSSLAPDSSF 446
QY 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNGRGTIPKPSLLKAAALIAGNADIGLGY 300
|||||
DB 447 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNGRGTIPKPSLLKAAALIAGNADIGLGY 506
QY 301 PNGNOGWGRVTLDKSLNVAIVNNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360
|||||
DB 447 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNGRGTIPKPSLLKAAALIAGNADIGLGY 506
QY 361 SVTLVNDLVLITAPNGTOYVGNDFTPYNDNWDGRNNVFNAPQSGTYYTIEVQAYN 420
|||||
DB 567 SVTLVNDLVLITAPNGTOYVGNDFTPYNDNWDGRNNVFNAPQSGTYYTIEVQAYN 626
QY 421 VPVGPQTFSLAIVN 434
|||||
DB 627 VPVGPQTFSLAIVN 640

RESULT 9

US-10-784-870-6
; Sequence 6, Application US/10784870
; Publication No. US20040142837A1
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUW
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT APPLICATION NUMBER: US/10/784,870
; CURRENT FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: US/09/509,814A
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-784-870-6

Query Match 99.6%; Score 2242; DB 4; Length 640;
Best Local Similarity 99.8%; Pred. No. 3.4e-170;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGOGQIVAVADTGLDTRNDSSMHEAPRGKITIYALGRTN 60
|||||

DB 207 NDVARGIVKADVAQSSYGLYGOGQIVAVADTGLDTRNDSSMHEAPRGKITIYALGRTN 266
QY 61 NANDTNGHGTTHVAGSVLGNSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
|||||
DB 267 NANDTNGHGTTHVAGSVLGNSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
|||||
DB 327 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 386
QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGPTFILSARSSLAPDSSF 240
|||||
DB 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGPTFILSARSSLAPDSSF 446
QY 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNGRGTIPKPSLLKAAALIAGNADIGLGY 300
|||||
DB 447 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNGRGTIPKPSLLKAAALIAGNADIGLGY 506
QY 301 PNGNOGWGRVTLDKSLNVAIVNNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360
|||||
DB 507 PNGNOGWGRVTLDKSLNVAIVNNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 566
QY 361 SVTLVNDLVLITAPNGTOYVGNDFTPYNDNWDGRNNVFNAPQSGTYYTIEVQAYN 420
|||||
DB 567 SVTLVNDLVLITAPNGTOYVGNDFTPYNDNWDGRNNVFNAPQSGTYYTIEVQAYN 626
QY 421 VPVGPQTFSLAIVN 434
|||||
DB 627 VPVGPQTFSLAIVN 640

RESULT 10

US-10-820-712A-3
; Sequence 3, Application US/10820712A
; Publication No. US20050026804A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuyoshi
; APPLICANT: Izawa, Yoshifumi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Koyama, Shingo
; APPLICANT: Sato, Tsuyoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251701-USO
; CURRENT APPLICATION NUMBER: US/10/820,712A
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 2003-106708
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-820-712A-3

Query Match 99.6%; Score 2242; DB 5; Length 640;
Best Local Similarity 99.8%; Pred. No. 3.4e-170;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGOGQIVAVADTGLDTRNDSSMHEAPRGKITIYALGRTN 60
|||||
DB 207 NDVARGIVKADVAQSSYGLYGOGQIVAVADTGLDTRNDSSMHEAPRGKITIYALGRTN 266
QY 61 NANDTNGHGTTHVAGSVLGNSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
|||||
DB 267 NANDTNGHGTTHVAGSVLGNSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
|||||
DB 327 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 386
QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGPTFILSARSSLAPDSSF 240
|||||

||||| 387 TVGATENLRPSFGSYADNINHVAQSSRGPTKGRIKPDVMAPGTIFILSARSSLPDSSF 446
QY 241 WANHDSKYAYMGTSMATPIVAGNVAQALREHFVKRGITPKPSLLKAALIAGAADIIGLY 300
Db 447 WANHDSKYAYMGTSMATPIVAGNVAQALREHFVKRGITPKPSLLKAALIAGAADIIGLY 506
QY 301 PNGNGGWRVTLDKSLNAVYNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 507 PNGNGGWRVTLDKSLNAVYNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 566
QY 361 SVTLVNDLDLVTAPNGTQYVGNDFTSYNDNWDGRNNVNFVFINAPQSGTITIEVQAYN 420
Db 567 SVTLVNDLDLVTAPNGTQYVGNDFTSYNDNWDGRNNVNFVFINAPQSGTITIEVQAYN 626
QY 421 VPVGPQTFSLAIVN 434
Db 627 VPVGPQTFSLAIVN 640
RESULT 11
US-10-820-714A-3
; Sequence 3, Application US/10820714A
; Publication No. US20050214922A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuoyoshi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Sumitomo, Nobuyuki
; APPLICANT: Takimura, Yasushi
; APPLICANT: Sato, Tsuyoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251697USO
; CURRENT APPLICATION NUMBER: US/10/820,714A
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 2003-106709
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 3
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP43
US-10-820-714A-3
Query Match 99.6%; Score 2242; DB 5; Length 640;
Best Local Similarity 99.8%; Pred. No. 3.4e-170;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 207 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 266
QY 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 267 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
QY 121 AGARITHNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 327 AGARITHNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
QY 181 TVGATENLRPSFGSYADNINHVAQSSRGPTKGRIKPDVMAPGTIFILSARSSLPDSSF 240
Db 387 TVGATENLRPSFGSYADNINHVAQSSRGPTKGRIKPDVMAPGTIFILSARSSLPDSSF 446
QY 241 WANHDSKYAYMGTSMATPIVAGNVAQALREHFVKRGITPKPSLLKAALIAGAADIIGLY 300
Db 447 WANHDSKYAYMGTSMATPIVAGNVAQALREHFVKRGITPKPSLLKAALIAGAADIIGLY 506
QY 301 PNGNGGWRVTLDKSLNAVYNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 507 PNGNGGWRVTLDKSLNAVYNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 566

QY 361 SVTLVNDLDLVTAPNGTQYVGNDFTSYNDNWDGRNNVNFVFINAPQSGTITIEVQAYN 420
Db 567 SVTLVNDLDLVTAPNGTQYVGNDFTSYNDNWDGRNNVNFVFINAPQSGTITIEVQAYN 626
QY 421 VPVGPQTFSLAIVN 434
Db 627 VPVGPQTFSLAIVN 640
RESULT 12
US-10-456-479-11
; Sequence 11, Application US/10456479
; Publication No. US20040072321A1
; GENERAL INFORMATION:
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: TAKIMURA, YASUSHI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: NOMURA, MASAFUMI
; APPLICANT: KOBAYASHI, TOHRU
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 238700USO
; CURRENT APPLICATION NUMBER: US/10/456,479
; CURRENT FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: JP 2002-186387
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: JP 2002-304232
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 11
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-KP9865
US-10-456-479-11
Query Match 99.4%; Score 2237; DB 4; Length 434;
Best Local Similarity 99.5%; Pred. No. 5.1e-170;
Matches 432; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQHSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NANDTNGHGTTHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARITHNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 121 AGARITHNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSYADNINHVAQSSRGPTKGRIKPDVMAPGTIFILSARSSLPDSSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQSSRGPTKGRIKPDVMAPGTIFILSARSSLPDSSF 240
QY 241 WANHDSKYAYMGTSMATPIVAGNVAQALREHFVKRGITPKPSLLKAALIAGAADIIGLY 300
Db 241 WANHDSKYAYMGTSMATPIVAGNVAQALREHFVKRGITPKPSLLKAALIAGAADIIGLY 300
QY 301 PNGNGGWRVTLDKSLNAVYNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 301 PNGNGGWRVTLDKSLNAVYNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360
QY 361 SVTLVNDLDLVTAPNGTQYVGNDFTSYNDNWDGRNNVNFVFINAPQSGTITIEVQAYN 420
Db 361 SVTLVNDLDLVTAPNGTQYVGNDFTSYNDNWDGRNNVNFVFINAPQSGTITIEVQAYN 420
QY 421 VPVGPQTFSLAIVN 434
Db 421 VPVGPQTFSLAIVN 434

RESULT 13

US-10-820-712A-14
; Sequence 14, Application US/10820712A
; Publication No. US20050026804A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuoyoshi
; APPLICANT: Izawa, Yoshifumi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Koyama, Shingo
; APPLICANT: Sato, Teuyoshi
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251701-USO
; CURRENT APPLICATION NUMBER: US/10/820, 712A
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 2003-106708
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-9865
US-10-820-712A-14

Query Match 99.4%; Score 2237; DB 5; Length 434;
Best Local Similarity 99.5%; Pred. No. 5.1e-170;
Matches 432; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGQGI VAVADTGLDTRNDSSMHEAFRGKITALYALGRN 60
DB 1 NDVARGIVKADVAQHSYGLYGQGI VAVADTGLDTRNDSSMHEAFRGKITALYALGRN 60

QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120

QY 121 AGARHTNSWGAANVAGYTTDSRNVDDYVRKNDMTILFAAGNEGPGGTISAPGTAKNAI 180
DB 121 AGARHTNSWGAANVAGYTTDSRNVDDYVRKNDMTILFAAGNEGPGGTISAPGTAKNAI 180

QY 181 TVGATENLRPSFGSYADNINHVAQFSRGTGKGRIPKDVMAPGTIFLSARSSLAPDSSF 240
DB 181 TVGATENLRPSFGSYADNINHVAQFSRGTGKGRIPKDVMAPGTIFLSARSSLAPDSSF 240

QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGIITPKPSLLKAALIAGAADI GLGY 300
DB 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGIITPKPSLLKAALIAGAADI GLGY 300

QY 301 PNGNQGWRVTLDKSLNVAYNNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360
DB 301 PNGNQGWRVTLDKSLNVAYNNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360

QY 361 SVTLVNDLVLITAPNGTOYVGNDFTPYNDNDWGRNNVNFVINAPOSGTYYTIEVOAYN 420
DB 361 SVTLVNDLVLITAPNGTOYVGNDFTPYNDNDWGRNNVNFVINAPOSGTYYTIEVOAYN 420

QY 421 VPVGPQTFFSLAIVN 434
DB 421 VPVGPQTFFSLAIVN 434

RESULT 14

US-10-820-714A-15
; Sequence 15, Application US/10820714A
; Publication No. US20050214922A1
; GENERAL INFORMATION:
; APPLICANT: KAO CORPORATION
; APPLICANT: Okuda, Mitsuoyoshi
; APPLICANT: Kobayashi, Tohru
; APPLICANT: Sumitomo, Nobuyuki
; APPLICANT: Takimura, Yasushi
; APPLICANT: Sato, Teuyoshi

; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 251697USO
; CURRENT APPLICATION NUMBER: US/10/820, 714A
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 2003-106709
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-9865
US-10-820-714A-15

Query Match 99.4%; Score 2237; DB 5; Length 434;
Best Local Similarity 99.5%; Pred. No. 5.1e-170;
Matches 432; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQHSYGLYGQGI VAVADTGLDTRNDSSMHEAFRGKITALYALGRN 60
DB 1 NDVARGIVKADVAQHSYGLYGQGI VAVADTGLDTRNDSSMHEAFRGKITALYALGRN 60

QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120

QY 121 AGARHTNSWGAANVAGYTTDSRNVDDYVRKNDMTILFAAGNEGPGGTISAPGTAKNAI 180
DB 121 AGARHTNSWGAANVAGYTTDSRNVDDYVRKNDMTILFAAGNEGPGGTISAPGTAKNAI 180

QY 181 TVGATENLRPSFGSYADNINHVAQFSRGTGKGRIPKDVMAPGTIFLSARSSLAPDSSF 240
DB 181 TVGATENLRPSFGSYADNINHVAQFSRGTGKGRIPKDVMAPGTIFLSARSSLAPDSSF 240

QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGIITPKPSLLKAALIAGAADI GLGY 300
DB 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGIITPKPSLLKAALIAGAADI GLGY 300

QY 301 PNGNQGWRVTLDKSLNVAYNNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360
DB 301 PNGNQGWRVTLDKSLNVAYNNESSLSSTSQATYSFTATAGKPLKISLVWSDAPASTTA 360

QY 361 SVTLVNDLVLITAPNGTOYVGNDFTPYNDNDWGRNNVNFVINAPOSGTYYTIEVOAYN 420
DB 361 SVTLVNDLVLITAPNGTOYVGNDFTPYNDNDWGRNNVNFVINAPOSGTYYTIEVOAYN 420

QY 421 VPVGPQTFFSLAIVN 434
DB 421 VPVGPQTFFSLAIVN 434

RESULT 15

US-09-920-954-8
; Sequence 8, Application US/09920954
; Publication No. US20020064854A1
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGIYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUW
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT APPLICATION NUMBER: US/09/920, 954
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/509, 814
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570

; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-920-954-8

Query Match		99.4%;	Score 2237;	DB 3;	Length 640;
Best Local Similarity		99.5%;	Pred. No. 8.6e-170;		
Matches	432;	Conservative	0;	Mismatches	2; Indels 0; Gaps 0;

Qy	1	NDVARGIVKADVAQHSYGLYGQGI	VAVADTGLDTCGRNDSMHEAF	RGKITALYALGRTN	60
Db	207	NDVARGIVKADVAQHSYGLYGQGI	VAVADTGLDTCGRNDSMHEAF	RGKITALYALGRTN	266
Qy	61	NANDTNGHGHVAGSVLGNSTNKG	MAPQANLVFQSIMDSGGGLGGL	PSNLQTLFSQAYS	120
Db	267	NANDTNGHGHVAGSVLGNSTNKG	MAPQANLVFQSIMDSGGGLGGL	PSNLQTLFSQAYS	326
Qy	121	AGARIHTNSWGAAVNGAYTTDS	RNVDDYVRKNDMTILFAAGNE	GPNGGTISAPGTAKNAI	180
Db	327	AGARIHTNSWGAAVNGAYTTDS	RNVDDYVRKNDMTILFAAGNE	GPNGGTISAPGTAKNAI	386
Qy	181	TVGATENLRPSFGSYADNINHV	AQFSSRGPTTKDGRIKPDVMA	PGTFILSARSSLAPDSSF	240
Db	387	TVGATENLRPSFGSYADNINHV	AQFSSRGPTTKDGRIKPDVMA	PGTFILSARSSLAPDSSF	446
Qy	241	WANHDSKYAYMGGTSMATPIV	AGNVAQLREHFVKNRGITPKP	SLLKAALIAGAADIGLGY	300
Db	447	WANHDSKYAYMGGTSMATPIV	AGNVAQLREHFVKNRGITPKP	SLLKAALIAGAADIGLGY	506
Qy	301	PNGNQGWGRVTLDKSLNVA	YVNESSLSSTSQATYSFTAT	ACKPLKISLVWSDAPASTTA	360
Db	507	PNGNQGWGRVTLDKSLNVA	YVNESSLSSTSQATYSFTAT	ACKPLKISLVWSDAPASTTA	566
Qy	361	SVTLVNDLVLITAPNGTOY	VGNDFTSPYNDNWDGRNNV	ENVFINAPQSGTYTIEVQAYN	420
Db	567	SVTLVNDLVLITAPNGTOY	VGNDFTSPYNDNWDGRNNV	ENVFINAPQSGTYTIEVQAYN	626
Qy	421	VPVGPQTFSLAIVN	434		
Db	627	VPVGPQNFSLAIVN	640		

Search completed: April 7, 2006, 09:35:20
Job time : 83 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 7, 2006, 09:35:35 ; Search time 17 Seconds
(without alignments)
796.313 Million cell updates/sec

Title: US-10-820-714A-1-HIS15

Perfect score: 2251

Sequence: 1 NDVARGIVKADVAHQSYGLY.....EQVAYNPVGPOTFSLAIVN 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

1: /SID55/ptodata/1/pubpaa/US08_NEW_PUB_PEP.*
2: /SID55/ptodata/1/pubpaa/US06_NEW_PUB_PEP.*
3: /SID55/ptodata/1/pubpaa/US07_NEW_PUB_PEP.*
4: /SID55/ptodata/1/pubpaa/PCT_NEW_PUB_PEP.*
5: /SID55/ptodata/1/pubpaa/US09_NEW_PUB_PEP.*
6: /SID55/ptodata/1/pubpaa/US10_NEW_PUB_PEP.*
7: /SID55/ptodata/1/pubpaa/US11_NEW_PUB_PEP.*
8: /SID55/ptodata/1/pubpaa/US60_NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	285.5	12.7	802	US-10-510-386-2	Sequence 2, Appli
2	253.5	11.3	272	US-11-020-602-236	Sequence 236, App
3	253	11.2	874	US-10-510-386-28	Sequence 28, Appl
4	253	11.2	1047	US-10-510-386-200	Sequence 200, App
5	248.5	11.0	269	US-11-020-602-6	Sequence 6, Appli
6	244.5	10.9	275	US-11-065-943-54	Sequence 54, Appl
7	244.5	10.9	275	US-11-020-602-3	Sequence 3, Appli
8	232.5	10.3	275	US-11-020-602-4	Sequence 4, Appli
9	230.5	10.2	274	US-11-156-062-14	Sequence 14, Appl
10	229.5	10.2	274	US-11-156-062-12	Sequence 12, Appl
11	229.5	10.2	379	US-11-156-062-23	Sequence 23, Appl
12	228.5	10.2	274	US-11-020-602-5	Sequence 5, Appli
13	228.5	10.2	382	US-11-020-602-2	Sequence 2, Appli
14	225.5	10.0	274	US-11-156-062-4	Sequence 4, Appli
15	225.5	10.0	274	US-11-156-062-8	Sequence 8, Appli
16	225.5	10.0	1052	US-11-020-602-208	Sequence 208, App
17	224.5	10.0	274	US-11-156-062-10	Sequence 10, Appl
18	223.5	9.9	274	US-11-156-062-6	Sequence 6, Appli
19	220.5	9.8	274	US-11-156-062-16	Sequence 16, Appl
20	220.5	9.8	274	US-11-156-062-18	Sequence 18, Appl
21	219.5	9.8	274	US-11-156-062-2	Sequence 2, Appli
22	209.5	9.3	280	US-11-020-602-209	Sequence 209, App
23	205	9.1	1432	US-10-510-386-218	Sequence 218, App
24	203	9.0	1447	US-11-052-554A-260	Sequence 260, App
25	180.5	8.0	740	US-11-096-568A-24714	Sequence 24714, A

ALIGNMENTS

RESULT 1

US-10-510-386-2
; Sequence 2, Application US/10510386
; Publication NO. US2005024922A1
; GENERAL INFORMATION:

; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2

; LENGTH: 802
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
; US-10-510-386-2

Query Match 12.7%; Score 285.5; DB 6; Length 802;
Best Local Similarity 23.0%; Pred. No. 5e-13;
Matches 143; Conservative 69; Mismatches 178; Indels 231; Gaps 27;

QY	2	DVARGIVKADVAHQSYGLYGGQIVAVADTGLDTGRND-SSMHEAPRGK--ITALYALGR	58
DB	158	DKSAFFIGADQAWKS-GVTGKGIKVAVIDTGVDTHTPDLKNNFPGYKGYDFVDNDYDPOE	216
QY	59	TNNANDTNG---HGHVAGSVLNGSTKGMAPQANLIFQSIWDSGGGLGGLPSNLQTLF	115
DB	217	TPTGPRGGATDHGTHVAGTIAAAGQI-KGVAPEATLLAYRVLPGG--SGTTENVIAGI	273
QY	116	SOAYSAGARIHTNSGAAVNGA-YTTDSRNVDYVYRKNDMTILFAAGNEGPNGTISAPG	174
DB	274	EKAVADGAKVMNLSLNSLNSPDYATSI--ALDWAAGVAVTSNGNSGPNWTVGSPG	331
QY	175	TAKNAITVGTATE-----NLRFSPFGS-----	194
DB	332	TSRVAISVGSQLPYNEYSVTLPSSYSSAKVMGYQBEKDLALNGQSVLVEAGLGQADD	391
QY	195	-----YADNINH-----	201
DB	392	SGKDYKGVAVIQGVIPFVDKAENAKNAGATCAVIYNNATGEIEANVMGMAVPTVKLSK	451
QY	202	-----VAQFSRGPTKD-GRIKPDVMAPTGTFILSA	230

Db 452 BEGEKLVQIQKEGRHSVVFSEFKLDKKLGETIASFSRGPVMDTMMIKPDVSPAGVNIYST 511
QY 231 RSSLAPDSFWANHDSK-----YAYMGTSMTPIVAGNVAQLREHFVKNRGITP--KPSL 284
Db 512 IPT-----HDPKPYGSGTGTSMASPHVAGTAALKQ-----AKPDWTPEQ 554
QY 285 LKAALIAGAADI-----GLGYPNGNOGWRVTLDKSLNAVYNNESS----- 326
Db 555 IKGVLMTAEKLTDENGKPLPHNTQGAGSIRIMEALKASSIVTPGSHSVGTFLDKGKQT 614
QY 327 -----LTSQKA-----TYSFTATACKPLKISLWSD-----APASTT-----ASVTLVNDL 368
Db 615 KQAPTIENLSHRKAYOLEYFKGTG-----ITVSGTERVVVPANQTKAAAKVTVNSA 669
QY 369 DLVITAPNGTVGVNDFTSPYNDNDGRNNVE---NVFINAP-----QSGT 411
Db 670 KTKAGTYEGTVYIRE-----DGRKVAEIPILLIVKEPDYPRVTSVTVPEGAKQGA 719
QY 412 YTIEVQAYNVVPGPQTFSIAI 432
Db 720 YTIE--AY-LPGAEELAPLV 737

RESULT 2

US-11-020-602-236
; Sequence 236, Application US/11020602
; Publication No. US20060024764A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David
; APPLICANT: Harding, Fiona
; TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND
; TITLE OF INVENTION: METHODS OF MAKING AND USING THE SAME
; FILE REFERENCE: GC527C2
; CURRENT APPLICATION NUMBER: US/11/020,602
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 09/500,135
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: US 09/060,872
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 236
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hybrid of
; OTHER INFORMATION: Bacillus lentus and Bacillus amyloliquefaciens
US-11-020-602-236

Query Match 11.3%; Score 253.5; DB 7; Length 272;
Best Local Similarity 32.9%; Pred. No. 2.6e-11;
Matches 85; Conservative 32; Mismatches 94; Indels 47; Gaps 10;
QY 13 AQHSLYGLGOGQIVAVADTGLDTRNDSSMHEAFRGKITALLYALGRTNNANDTNGHGTHTV 72
Db 15 AAHNRGLTSGVKVAVLDTGIST-----HFDLNRGASFPVGEPTQDNGHGTHTV 66
QY 73 AGSV--LNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLTQFSAQVSAAGARIHTNSW 130
Db 67 AGTIAALNNSIGVLGVAPSAELYAVKVLGASG--SGSVSSIAQGLEWAGNNGMHVINMSL 124
QY 131 GAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGNG--GTISAPCTAKNAITVGATENL 188
Db 125 GGSGLAAL-----KAAVADKAVASGVVWVAAGNEGTSGLSSTVYGPVKYPSVIAVGA---- 176
QY 189 RPSFGSYADNINHVAQFSRGTGDKRIKPDVMAPTFTLSARSSLAPDSFWANHDSKY 248
Db 177 -----VDSSNQRASFSVGP-----ELDVWAPG---VSIQSTLP-----GNKY 211
QY 249 AYMGGTSMATPIVAGNVA 266
Db 212 GAYNGTSMASPHVAGAAA 229

RESULT 3

US-10-510-386-28
; Sequence 28, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 28
; LENGTH: 874
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-28

Query Match 11.2%; Score 253; DB 6; Length 874;
Best Local Similarity 27.2%; Pred. No. 1.3e-10;
Matches 95; Conservative 51; Mismatches 129; Indels 74; Gaps 13;
QY 25 IVAVADTGLDTRNDSSMHEAFRGKI-----TALYALGRTNNANDTNGHGTHTVAGSVLG--- 78
Db 447 VIAVVDTVGDHTLADLS-----GSVKDEGYNVYVGRADAMDDRGHGTHTVSGIIAAAQD 500
QY 79 NGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLTQFSAQVSAAGARIHTNSMGAAVNGAY 138
Db 501 NHFSVAGINAVAKILPVKVLDSG--SGDTEQIANGIYIADHGAKVINLSLG-----GYP 554
QY 139 TTDSRNVDDYVRKNDMTILFAAGNEGNGGTISAPCTAKNAITVGATENLRPSFGSYADN 198
Db 555 SRVMEYALKYAAASKNVTIVAATGNDGVS--EISYPASSKYTLVSGATNNL----- 602
QY 199 INHVAQFSRGTGDKRIKPDVMAPTFTLSARSSLAPDSFWANHDSKYAVMGTSMAT 258
Db 603 -DLVSDSYNYGKGL-----DMVAPGTDI-----PSLVDPDN-----VTYMSGTSM 643
QY 259 PIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGL---GYPNGN----- 304
Db 644 PHVAAAAGLL-----LSQNPSLKPKQIASLLTETTDVAFERQDNPNPDYDLIDBPAAQI 698
QY 305 -----QGWGRVTLDKSLNAVYNNESSSLSTSQKATYGTATAGKPLKI 347
Db 699 PGYDFVSGWGLNVFHAASVPFELNMKVHPLNRHTAVTGTAKSGVTVKI 747

RESULT 4

US-10-510-386-200
; Sequence 200, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 200
; LENGTH: 1047
; TYPE: PRT
; ORGANISM: Bacillus licheniformis


```
; CURRENT APPLICATION NUMBER: US/11/156.062
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: PCT/EP2003/014127
; PRIOR FILING DATE: 2003-12-20
; PRIOR APPLICATION NUMBER: DE 102 60 903.9
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 274
; TYPE: PRF
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; US-11-156-062-12

Query Match          10.2%; Score 229.5; DB 7; Length 274;
Best Local Similarity 30.6%; Pred. No. 1.5e-09;
Matches      86; Conservative    35; Mismatches   107; Indels     53; Gaps       11;

Qy  7 IVKADVAQHSGYGLYGOGQIVAVADTGLDGTGRNDSSMHEAFRGKITLYALGRTNNANDTN 66
    : : ||| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 10 LIRAKDKVQ-AQGPKGANVKVAVLDTGIQAHPDLNVVG-----ASFVAGEAYNA-DGN 61

Qy  67 GHGTHVAGSV--LNGSTNKGMAPOANLVPOSIMDSGGGLGCLPSNIQTFLFSQAYSAGAR 124
    : : ||| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 62 GHGTHVAGTVAAALNTTTGVLGAPASVSYSYAVKVLDSSG--SGSYSIGVIGIEWATTNGMD 119

Qy 125 IHTNSMGAAVNAGVTSDSRVVDDVVRKNDMTILFAAGNEGPNG--GTISAPGTAKNAITV 182
    : : ||| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 120 VINMSUGGA---SGSTAMKKOAVDNAYARGVVVAAAAGNSSGSNTWTITGYPAKYDVIAV 176

Qy 183 GATENLRPSPFGSYADINNHVAQFSSRGPRTKDGRIKPDVPMPGTFILSARSSLAPDSSFWA 242
    : ||| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 177 GA-----VDSNSNRASFSSVG-----AELEVMAPGACGVYSTYPT----- 210

Qy 243 NHPSKYAIMGTSMTATPIVAGNVA-----QLREHFVKNR 276
    : ||| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 211 ---NTYATWGTSMASHPVAGAAAAIILSKHPLNSASOVNRN 248


RESULT 11
US-11-156-062-23
; Sequence 23, Application US/11/156.062
; Publication No. US20050281773A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Susanne
; APPLICANT: Polanyi-Bald, Laura
; APPLICANT: Pruesser, Inken
; APPLICANT: Stehr, Regina
; APPLICANT: Maurer, Karl-Heinz
; TITLE OF INVENTION: SUBSTITUENT VARIANTS, WITH IMPROVED PERHYDROLASE ACTIVITY
; FILE REFERENCE: HENK-0134 / HS698
; CURRENT APPLICATION NUMBER: US/11/156.062
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: PCT/EP2003/014127
; PRIOR FILING DATE: 2003-12-20
; PRIOR APPLICATION NUMBER: DE 102 60 903.9
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 379
; TYPE: PRF
; ORGANISM: Bacillus licheniformis
; US-11-156-062-23

Query Match          10.2%; Score 229.5; DB 7; Length 379;
Best Local Similarity 30.2%; Pred. No. 2.2e-09;
Matches      85; Conservative    37; Mismatches   106; Indels     53; Gaps       11;

Qy  7 IVKADVAQHSGYGLYGOGQIVAVADTGLDGTGRNDSSMHEAFRGKITLYALGRTNNANDTN 66
    : : ||| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
```

	212	--SW--IINGIEWAJANNMDVINMISLGGPSGSAAALKAAVDKAVASGVVVVAAAAGNEXG	266
Db			
	167	G-GTTTSAGCTAKNAITVGATENLRSPFSGYADNIHVAQFSSRGPTKDGRIRPDIWMAFG	224
Qy		: : : : : :	
	267	GSSTTGYGPKYPSVIAVGA-----VDSSNORASFSSVGP-----ELDVNMPG	309
Db			
	225	TETLSARSLAPDSSFWANHDSKYAYMGGTSMATPIVAGNVA	266
Qy		: : : : : :	
	310	--VS-TOSTLP-----GNKYGAYNGTSMASPHVAGAAA	339
Db		: : : : : :	

```

RESULT 14
US-11-156-062-4
; Sequence 4, Application US/11156062
; Publication No. US20050281773A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Susanne
; APPLICANT: Polanyi-Bald, Laura
; APPLICANT: Prueser, Inken
; APPLICANT: Stehr, Regina
; APPLICANT: Maurer, Karl-Heinz
; TITLE OF INVENTION: SUBTILISIN VARIANTS, WITH IMPROVED PERHYDROLASE ACTIVITY
; FILE REFERENCE: HENK-0134 / HS698
; CURRENT APPLICATION NUMBER: US/11/156,062
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: PCT/EP2003/014127
; PRIOR FILING DATE: 2003-12-20
; PRIOR APPLICATION NUMBER: DE 102 60 903.9
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-156-062-4

```

```

Qy      243  NHDSKYAYMGGTSMATPIVAGNVA-----QLREHFVKOR  276
      : ||      |||||: ||| |      | : ||
Db      211  ---NTYATWDGTSWASPHVAGAAALILSKHPNLSASQVRNR  248

RESULT 15
US-11-156-062-8
; Sequence 8, Application US/11156062
; Publication No. US20050281773A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Susanne
; APPLICANT: Polanyi-Bald, Laura
; APPLICANT: Prueser, Inken
; APPLICANT: Stehr, Regina

```

```

: APPLICANT: Maurer, Karl-Heinz
: TITLE OF INVENTION: SUBSTITILIN VARIANTS, WITH IMPROVED PERHYDROLASE ACTIVITY
: FILE REFERENCE: HENK-0134 / H5698
: CURRENT APPLICATION NUMBER: US/11/156,062
: CURRENT FILING DATE: 2005-06-17
: PRIOR APPLICATION NUMBER: PCT/EP2003/014127
: PRIOR FILING DATE: 2003-12-20
: PRIOR APPLICATION NUMBER: DE 102 60 903.9
: PRIOR FILING DATE: 2002-12-20
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 8
: LENGTH: 274
: TYPE: PRT
: ORGANISM: Artificial
: FEATURE:
: OTHER INFORMATION: Synthetic Construct
: US-11-156-062-8

```

Query Match	10.0%;	Score	225.5;	DB	7;	Length	274;
Best Local Similarity	29.5%;	Pred. No.	2.8e-09;				
Matches	85;	Conservative	36;	Mismatches	100;	Indels	67;
						Gaps	12;
Qy	7	IVKADVQAQHSYGLYGGQIIVAVADTGLDTGRNDSMHEAFRGKITALYALGRTNANDTN	66				
Db		: : :	: : :	: : :	: : :	: : :	: : :
Db	10	LIRADKVKQV-AQGFKGANVKVAVLDTGTQIASHPDLNVVGG-----ASFVAGEAYNA-DGN	61				
Qy	67	GHGTHVAGSV--LGNGSTNKGMAPQANLVQSGTMDS--GGGLGGLPSNLQTLFSQ-----	117				
Db	62	GHGTHVAGTVAALDNTTGVLGVAQPSVSLYAVKVLNSSGSGSYSGIVSGIEWATTNDMDVI	121				
Qy	118	AYSAGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNG--GTISAPGT	175				
Db	122	NMSLGGNSGTAMKQAVDNAYA-----RGVVVVAAGNSGSSGNTWTIYGPAP	169				
Qy	176	AKNAITVGATENLRPSFGSYADNINHVAQFSRGPTKDGRKIPDVWAGFTILSARSSLA	235				
Db	170	YDSVIAVGA-----VDSNSNRASFSSVG-----ALEVMAFGAGVSYTPT--	210				
Qy	236	PDSSFWANHDSKYAMGGTSMATPIVAGNVA-----QUREHFVKNR	276				
Db	211	-----NTYATWDGTSMASPHVAGAAALILSKHPNLSASOVNR	248				

Search completed: April 7, 2006, 09:36:00
Job time : 18 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 7, 2006, 09:40:30 ; Search time 29 Seconds
(without alignments)
1237.284 Million cell updates/sec

Title: US-10-820-714A-1

Perfect score: 2247

Sequence: 1 NDVARGIVKADVAQSSYGLY.....EVQAYNPVGPQTFLAIVN 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5 COMB.pep:*
- 2: /cgn2_6/prodata/1/iaa/6 COMB.pep:*
- 3: /cgn2_6/prodata/1/iaa/H COMB.pep:*
- 4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep:*
- 5: /cgn2_6/prodata/1/iaa/RE COMB.pep:*
- 6: /cgn2_6/prodata/1/iaa/backfilees1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2247	100.0	434	US-09-985-689A-1	Sequence 1, Appli
2	2247	100.0	640	US-09-509-814A-6	Sequence 6, Appli
3	2247	100.0	640	US-09-920-954-6	Sequence 6, Appli
4	2242	99.8	640	US-09-509-814A-8	Sequence 8, Appli
5	2242	99.8	640	US-09-920-954-8	Sequence 8, Appli
6	2191	97.5	434	US-09-985-689A-2	Sequence 2, Appli
7	2193	97.2	639	US-09-509-814A-4	Sequence 4, Appli
8	2183	97.2	639	US-09-920-954-4	Sequence 4, Appli
9	2155	95.9	639	US-09-509-814A-1	Sequence 1, Appli
10	2155	95.9	639	US-09-920-954-1	Sequence 1, Appli
11	2155	95.9	640	US-09-509-814A-2	Sequence 2, Appli
12	2155	95.9	640	US-09-920-954-2	Sequence 2, Appli
13	2143	95.4	434	US-09-985-689A-6	Sequence 6, Appli
14	2125.5	94.6	433	US-09-985-689A-7	Sequence 7, Appli
15	2125.5	94.6	641	US-08-873-479-42	Sequence 42, Appli
16	1998.5	88.9	433	US-09-985-689A-5	Sequence 5, Appli
17	1994.5	88.8	433	US-09-985-689A-3	Sequence 3, Appli
18	1987.5	88.5	433	US-09-985-689A-4	Sequence 4, Appli
19	1986.5	88.4	433	US-09-104-623A-4	Sequence 4, Appli
20	1986.5	88.4	433	US-09-019-532-4	Sequence 4, Appli
21	1986.5	88.4	433	US-09-338-746-4	Sequence 4, Appli
22	1986.5	88.4	635	US-08-873-479-43	Sequence 43, Appli
23	1581.5	70.4	345	US-09-512-251A-10	Sequence 10, Appli
24	1581.5	70.4	345	US-09-515-150A-10	Sequence 10, Appli
25	1581.5	70.4	345	US-09-196-281-13	Sequence 13, Appli
26	1581.5	70.4	345	US-10-336-324-10	Sequence 10, Appli
27	452.5	20.1	659	US-08-894-818B-1	Sequence 1, Appli

Sequence 12, Appli
Sequence 12, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 35, Appli
Sequence 5, Appli
Sequence 7, Appli
Sequence 4, Appli

28 452.5 20.1 659 2 US-09-445-472-12
29 452.5 20.1 659 2 US-10-090-624-12
30 452.5 20.1 659 2 US-09-841-553-1
31 414 18.4 412 2 US-09-445-472-1
32 414 18.4 412 2 US-10-090-624-1
33 414 18.4 522 2 US-08-894-818B-3
34 414 18.4 522 2 US-09-445-472-4
35 414 18.4 522 2 US-10-090-624-4
36 414 18.4 522 2 US-08-841-553-3
37 414 18.4 654 2 US-08-894-818B-35
38 414 18.4 654 2 US-09-445-472-16
39 414 18.4 654 2 US-10-090-624-16
40 414 18.4 654 2 US-09-841-553-35
41 401 17.8 659 2 US-08-894-818B-5
42 401 17.8 659 2 US-09-841-553-3
43 346 15.4 520 2 US-09-000-016-7
44 346 15.4 520 2 US-09-514-340-7
45 346 15.4 734 2 US-09-000-016-4

ALIGNMENTS

RESULT 1

US-09-985-689A-1

; Sequence 1, Application US/09985689A

; Patent No. 6803222

; GENERAL INFORMATION:

; APPLICANT: HATADA, YUJI

; APPLICANT: OGAWA, AKINORI

; APPLICANT: KAGEYAMA, YASUSHI

; APPLICANT: SATO, TSUYOSHI

; APPLICANT: ARAKI, HIROYUKI

; APPLICANT: SUMITOMO, NOBUYUKI

; APPLICANT: OKUDA, MITSUYOSHI

; APPLICANT: SAEKI, KATSUHISA

; TITLE OF INVENTION: Alkaline proteases

; FILE REFERENCE: 215483050

; CURRENT APPLICATION NUMBER: US/09/985,689A

; CURRENT FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: JP P2000-355166

; PRIOR FILING DATE: 2000-11-22

; PRIOR APPLICATION NUMBER: JP P2001-114048

; PRIOR FILING DATE: 2001-04-12

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 434

; TYPE: PRT

; ORGANISM: Bacillus sp.

US-09-985-689A-1

Query Match 100.0%; Score 2247; DB 2; Length 434;

Best Local Similarity 100.0%; Pred. No. 6.9e-176;

Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGGQIVAVADTGLDGTGRNDSMHAEAFRGKITAYALGRTN 60
|||||
1 NDVARGIVKADVAQSSYGLYGGQIVAVADTGLDGTGRNDSMHAEAFRGKITAYALGRTN 60
QY 61 NANDTNGHGHVAGSVLGNSTNGKMAPOANLVFQSGGGLGGLPSNLQTLFSQAYS 120
61 NANDTNGHGHVAGSVLGNSTNGKMAPOANLVFQSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARHTNSWGAANGVAYTTDSNRNDDYVRKNDMTLLFAAGNEGPNNGTISAPGTAKNAI 180
121 AGARHTNSWGAANGVAYTTDSNRNDDYVRKNDMTLLFAAGNEGPNNGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSYADNINHVAFSSRGPTKDGRIKPDVMAFGTIFILGARSLLAPDSF 240
181 TVGATENLRPSFGSYADNINHVAFSSRGPTKDGRIKPDVMAFGTIFILGARSLLAPDSF 240
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKALIAGAADIGLGY 300

Db 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
Qy 301 PNGNQGWGRVTLDKSLNVAYNNESSLSLTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 301 PNGNQGWGRVTLDKSLNVAYNNESSLSLTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
Qy 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWGDGRNNVNFINAPQSGTYYTIEVQAYN 420
Db 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDWGDGRNNVNFINAPQSGTYYTIEVQAYN 420
Qy 421 VPVGPQTFSLAIVN 434
Db 421 VPVGPQTFSLAIVN 434

RESULT 2

US-09-509-814A-6

; Sequence 6, Application US/09509814A

; Patent No. 6376227

; GENERAL INFORMATION:

; APPLICANT: TAKAIWA, MIKIO

; APPLICANT: OKUDA, MITSUYOSHI

; APPLICANT: SAEKI, KATSUHIISA

; APPLICANT: KUBOTA, HIROMI

; APPLICANT: HITOMI, JUN

; APPLICANT: KAGEYAMA, YASUSHI

; APPLICANT: SHIKATA, SHITSUM

; APPLICANT: NOMURA, MASAFUMI

; TITLE OF INVENTION: ALKALINE PROTEASE

; FILE REFERENCE: 0327-0832-OPCT

; CURRENT APPLICATION NUMBER: US/09/509,814A

; CURRENT FILING DATE: 2000-04-06

; PRIOR APPLICATION NUMBER: PCT/JP98/04528

; PRIOR FILING DATE: 1998-10-07

; PRIOR APPLICATION NUMBER: JP 9-274570

; PRIOR FILING DATE: 1997-06-08

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 6

; LENGTH: 640

; TYPE: PRT

; ORGANISM: Bacillus sp.

US-09-509-814A-6

Query Match 100.0%; Score 2247; DB 2; Length 640;

Best Local Similarity 100.0%; Pred. No. 1.2e-175;

Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTCGRNDSMHAEAFRGKITALLYALGRTN 60
Db 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTCGRNDSMHAEAFRGKITALLYALGRTN 266
Qy 61 NANTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 267 NANTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 326
Qy 121 AGARIHTNSGAAVNGAYTTDSNRVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 327 AGARIHTNSGAAVNGAYTTDSNRVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTIFLSARSSLAPDSSF 240
Db 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTIFLSARSSLAPDSSF 446
Qy 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
Db 447 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 506
Qy 301 PNGNQGWGRVTLDKSLNVAYNNESSLSLTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360
Db 507 PNGNQGWGRVTLDKSLNVAYNNESSLSLTSQKATYSFTATAGKPLKISLVWSDAPASTTA 566

Db 627 VPVGPQTFSIAVN 640
|||||

RESULT 4
US-09-509-814A-8
; Sequence 8, Application US/09509814A
; Patent No. 6376227
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUM
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT APPLICATION NUMBER: US/09/509,814A
; CURRENT FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-509-814A-8

Query Match 99.8%; Score 2242; DB 2; Length 640;
Best Local Similarity 99.8%; Pred. No. 3e-175;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	NDVARGIVKADVAQSSYGLYGQGI	VADTGLDTCGRNDSMHEAPRGKIT	IYALGRTN	60
Db	207	NDVARGIVKADVAQSSYGLYGQGI	VADTGLDTCGRNDSMHEAPRGKIT	IYALGRTN	266
QY	61	NANDTNGHGHVAGSVLNGSTNKG	MAPOANLVFQSIMDSGGGLGGLP	SNLQTLFSQAYS	120
Db	267	NANDTNGHGHVAGSVLNGSTNKG	MAPOANLVFQSIMDSGGGLGGLP	SNLQTLFSQAYS	326
QY	121	AGARIHTNSWGAANGAYTTDSRN	VDDYVRKNDMTILFAAGNEGPN	GGTISAPGTAKNAI	180
Db	327	AGARIHTNSWGAANGAYTTDSRN	VDDYVRKNDMTILFAAGNEGPN	GGTISAPGTAKNAI	386
QY	181	TVGATENLRPSFGSYADNINHVA	QFSSRGPTKDGRIKPDVMA	PGTIFLSARSLAPDSSF	240
Db	387	TVGATENLRPSFGSYADNINHVA	QFSSRGPTKDGRIKPDVMA	PGTIFLSARSLAPDSSF	446
QY	241	WANHDSKYAYMGTSNATPIVAG	NVAQLREHFVKNRGITPKPSLL	KAALIAGAADIGLGY	300
Db	447	WANHDSKYAYMGTSNATPIVAG	NVAQLREHFVKNRGITPKPSLL	KAALIAGAADIGLGY	506
QY	301	PNGNCGWGRVTLDKSLNVA	YVNESSLSSTSQATYSFTAT	AGKPLKISLVWSDAPASTTA	360
Db	507	PNGNCGWGRVTLDKSLNVA	YVNESSLSSTSQATYSFTAT	AGKPLKISLVWSDAPASTTA	566
QY	361	SVTLVNDLVLITAPNGTQYVGN	DFTSPYNDWNGRNNVFN	INAPQSGTYYTIEVQAYN	420
Db	567	SVTLVNDLVLITAPNGTQYVGN	DFTSPYNDWNGRNNVFN	INAPQSGTYYTIEVQAYN	626
QY	421	VPVGPQTFSIAVN	434		
Db	627	VPVGPQNFSLIAVN	640		

RESULT 5
US-09-920-954-8
; Sequence 8, Application US/09920954

Patent No. 6759228
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUM
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT APPLICATION NUMBER: US/09/920,954
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/509,814
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-920-954-8

Query Match 99.8%; Score 2242; DB 2; Length 640;
Best Local Similarity 99.8%; Pred. No. 3e-175;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	NDVARGIVKADVAQSSYGLYGQGI	VADTGLDTCGRNDSMHEAPRGKIT	IYALGRTN	60
Db	207	NDVARGIVKADVAQSSYGLYGQGI	VADTGLDTCGRNDSMHEAPRGKIT	IYALGRTN	266
QY	61	NANDTNGHGHVAGSVLNGSTNKG	MAPOANLVFQSIMDSGGGLGGLP	SNLQTLFSQAYS	120
Db	267	NANDTNGHGHVAGSVLNGSTNKG	MAPOANLVFQSIMDSGGGLGGLP	SNLQTLFSQAYS	326
QY	121	AGARIHTNSWGAANGAYTTDSRN	VDDYVRKNDMTILFAAGNEGPN	GGTISAPGTAKNAI	180
Db	327	AGARIHTNSWGAANGAYTTDSRN	VDDYVRKNDMTILFAAGNEGPN	GGTISAPGTAKNAI	386
QY	181	TVGATENLRPSFGSYADNINHVA	QFSSRGPTKDGRIKPDVMA	PGTIFLSARSLAPDSSF	240
Db	387	TVGATENLRPSFGSYADNINHVA	QFSSRGPTKDGRIKPDVMA	PGTIFLSARSLAPDSSF	446
QY	241	WANHDSKYAYMGTSNATPIVAG	NVAQLREHFVKNRGITPKPSLL	KAALIAGAADIGLGY	300
Db	447	WANHDSKYAYMGTSNATPIVAG	NVAQLREHFVKNRGITPKPSLL	KAALIAGAADIGLGY	506
QY	301	PNGNCGWGRVTLDKSLNVA	YVNESSLSSTSQATYSFTAT	AGKPLKISLVWSDAPASTTA	360
Db	507	PNGNCGWGRVTLDKSLNVA	YVNESSLSSTSQATYSFTAT	AGKPLKISLVWSDAPASTTA	566
QY	361	SVTLVNDLVLITAPNGTQYVGN	DFTSPYNDWNGRNNVFN	INAPQSGTYYTIEVQAYN	420
Db	567	SVTLVNDLVLITAPNGTQYVGN	DFTSPYNDWNGRNNVFN	INAPQSGTYYTIEVQAYN	626
QY	421	VPVGPQTFSIAVN	434		
Db	627	VPVGPQNFSLIAVN	640		

RESULT 6
US-09-985-689A-2
; Sequence 2, Application US/09985689A
; Patent No. 6803222
; GENERAL INFORMATION:
; APPLICANT: HATADA, YUJI
; APPLICANT: OGAWA, AKINORI
; APPLICANT: KAGEYAMA, YASUSHI

APPLICANT: SATO, TSUYOSHI
APPLICANT: ARAKI, HIROYUKI
APPLICANT: SUMITOMO, NOBUYUKI
APPLICANT: OKUDA, MITSUYOSHI
APPLICANT: SAEKI, KATSUHISA
TITLE OF INVENTION: Alkaline proteases
FILE REFERENCE: 215483US0
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: JP P2000-355166
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: JP P2001-114048
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 434
TYPE: PRT
ORGANISM: Bacillus sp.
US-09-985-689A-2

Query Match 97.5%; Score 2191; DB 2; Length 434;
Best Local Similarity 96.5%; Pred. No. 2.7e-171;
Matches 419; Conservative 13; Mismatches 2; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 60
DB 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 60
QY 61 NANDTNGHGHVAGSVLGNSTKMGAPQANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 61 NANDTNGHGHVAGSVLGNSTKMGAPQANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
QY 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
DB 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
QY 181 TVGATENLRPSFGSYADNINHVAQFSRGTGDKRIKPDVMAPGTPILSARSLAPDSSF 240
DB 181 TVGATENLRPSFGSYADNINHVAQFSRGTGDKRIKPDVMAPGTPILSARSLAPDSSF 240
QY 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADVLGY 300
DB 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADVLGY 300
QY 301 PNGNQGWGRVTLDKSLNVAYNNESSLSQKATYSTATAGKPLKISLVWSDAPASTTA 360
DB 301 PNGNQGWGRVTLDKSLNVAYNNESSLSQKATYSTATAGKPLKISLVWSDAPASTTA 360
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNWDGRNNVNFINAPQSGTYYTIEVOAYN 420
DB 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNWDGRNNVNFINAPQSGTYYTIEVOAYN 420
QY 421 VPVGPQTFSLAIYN 434
DB 421 VPVGPQTFSLAIYN 434

RESULT 7
US-09-509-814A-4
Sequence 4, Application US/09509814A
Patent No. 6376227
GENERAL INFORMATION:
APPLICANT: TAKAIWA, MIKIO
APPLICANT: OKUDA, MITSUYOSHI
APPLICANT: SAEKI, KATSUHISA
APPLICANT: KUBOTA, HIROMI
APPLICANT: HITOMI, JUN
APPLICANT: KAGEYAMA, YASUSHI
APPLICANT: SHIKATA, SHITSUMI
APPLICANT: NOMURA, MASAFUMI
TITLE OF INVENTION: ALKALINE PROTEASE
FILE REFERENCE: 0327-0832-0PCT

CURRENT APPLICATION NUMBER: US/09/509,814A
CURRENT FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: PCT/JP98/04528
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: JP 9-274570
PRIOR FILING DATE: 1997-06-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 639
TYPE: PRT
ORGANISM: Bacillus sp.
US-09-509-814A-4

Query Match 97.2%; Score 2183; DB 2; Length 639;
Best Local Similarity 96.3%; Pred. No. 2.1e-170;
Matches 418; Conservative 13; Mismatches 3; Indels 0; Gaps 0;

QY 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 60
DB 206 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGRNDSSMHEAFRGKITALYALGRTN 265
QY 61 NANDTNGHGHVAGSVLGNSTKMGAPQANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 266 NANDTNGHGHVAGSVLGNSTKMGAPQANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 325
QY 121 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 180
DB 326 AGARIHTNSWGAANGAYTTDSRNVDYVRKNDMTILFAAGNEGPNNGGTISAPGTAKNAI 385
QY 181 TVGATENLRPSFGSYADNINHVAQFSRGTGDKRIKPDVMAPGTPILSARSLAPDSSF 240
DB 386 TVGATENLRPSFGSYADNINHVAQFSRGTGDKRIKPDVMAPGTPILSARSLAPDSSF 445
QY 241 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADVLGY 300
DB 446 WANHDSKYAYMGTSMTATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADVLGY 505
QY 301 PNGNQGWGRVTLDKSLNVAYNNESSLSQKATYSTATAGKPLKISLVWSDAPASTTA 360
DB 506 PNGNQGWGRVTLDKSLNVAYNNESSLSQKATYSTATAGKPLKISLVWSDAPASTTA 565
QY 361 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNWDGRNNVNFINAPQSGTYYTIEVOAYN 420
DB 566 SVTLVNDLVLITAPNGTQYVGNDFTPSYNDNWDGRNNVNFINAPQSGTYYTIEVOAYN 625
QY 421 VPVGPQTFSLAIYN 434
DB 626 VPVGPQTFSLAIYN 639

RESULT 8
US-09-920-954-4
Sequence 4, Application US/09920954
Patent No. 6759228
GENERAL INFORMATION:
APPLICANT: TAKAIWA, MIKIO
APPLICANT: OKUDA, MITSUYOSHI
APPLICANT: SAEKI, KATSUHISA
APPLICANT: KUBOTA, HIROMI
APPLICANT: HITOMI, JUN
APPLICANT: KAGEYAMA, YASUSHI
APPLICANT: SHIKATA, SHITSUMI
APPLICANT: NOMURA, MASAFUMI
TITLE OF INVENTION: ALKALINE PROTEASE
FILE REFERENCE: 0327-0832-0PCT
CURRENT APPLICATION NUMBER: US/09/920,954
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 09/509,814
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: PCT/JP98/04528
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: JP 9-274570

```

; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 639
; TYPE: PR
; ORGANISM: Bacillus sp.
US-09-920-954-4

Query Match          97.28; Score 2183; DB 2; Length 639;
Best Local Similarity 96.34; Pred. No. 2.1e-170;
Matches 418; Conservative 13; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAGSSVGLYGGQIIVAVADTGLDTRNDSSMEHAPRGKITALYALGRTN 60
Db
Qy 206 NDVARGIVKADVAGSSVGLYGGQIIVAVADTGLDTRNDSSMEHAPRGKITALYALGRTN 265
Db
Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSSGGGLGGLPSNLQTLFQAYS 120
Db
Qy 266 NANDTNGHGHVAGSVLNGCATNKGMAPOANLVFQSIMDSSGGGLGGLPSNLQTLFQAFS 325
Db
Qy 121 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNPGNGGTTISAPGTAKNAI 180
Db
Qy 326 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNRPNGGTTISAPGTAKNAI 385
Db
Qy 181 TVGATENLRPFSGSYADNINHVAQFSRGPTKDGRIKPDVWAPGTFILSARSLAPDSSF 240
Db
Qy 386 TVGATENLRPFSGSYADNINHVAQFSRGPTKDGRIKPDVWAPGTFILSARSLAPDSSF 445
Db
Qy 241 WANHDSKYATMGCTSMATPIVAGNVAQLRHFVKNRGITPKPSLLKAAALITAGAADIGLGY 300
Db
Qy 446 WANHDSKYATMGCTSMATPIVAGNVAQLRHFVKNRGITPKPSLLKAAALITAGAADIGLGY 505
Db
Qy 301 PNGNQWGRVTLDKSLNVAIVNNESSLSQKATYFTATAGKPLKISLWSDAPASTTA 360
Db
Qy 506 PNGNQWGRVTLDKSLNVAIVNNESSLSQKATYFTATAGKPLKISLWSDAPASTTA 565
Db
Qy 361 SVTLVNDLDELITAPNGTVVGNDFTPSYNDNDGRNNVENFINAPOSCTYTTIEVQAYN 420
Db
Qy 566 SVTLVNDLDELITAPNGTRIVGNDFSPAPDNNNDGRNNVENFINPQSGTTYTTIEVQAYN 625
Db
Qy 421 VPVGPQTFSLAIYN 434
Db
626 VPVGPQNFSLAIYN 639

RESULT 9
US-09-509-814A-1
; Sequence 1, Application US/09509814A
; Patent No. 6376227
; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIKA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUM
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALKALINE PROTEASE
; FILE REFERENCE: 0327-0832-0PCT
; CURRENT APPLICATION NUMBER: US/09/509,814A
; CURRENT FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 639
; TYPE: PR
; ORGANISM: Bacillus sp.
```

```

; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (23)..(23)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (29)..(29)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (32)..(32)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (46)..(46)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (47)..(47)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (53)..(53)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (70)..(70)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (74)..(74)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (89)..(89)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (102)..(102)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (105)..(105)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (128)..(128)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (130)..(130)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (131)..(131)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (132)..(132)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (133)..(133)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (146)..(146)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (148)..(148)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (160)..(160)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (165)..(165)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (172)..(172)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (183)..(183)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (187)..(187)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (188)..(188)
; OTHER INFORMATION: Xaa is any amino acid
```


OTHER INFORMATION: Xaa	is any amino acid
NAME/KEY: misc feature	
LOCATION: (89)..(189)	
OTHER INFORMATION: Xaa	is any amino acid
NAME/KEY: misc feature	
LOCATION: (102)..(102)	
OTHER INFORMATION: Xaa	is any amino acid
NAME/KEY: misc feature	
LOCATION: (105)..(105)	
OTHER INFORMATION: Xaa	is any amino acid
NAME/KEY: misc feature	
LOCATION: (128)..(128)	
OTHER INFORMATION: Xaa	is any amino acid
NAME/KEY: misc feature	
LOCATION: (130)..(130)	
OTHER INFORMATION: Xaa	is any amino acid
NAME/KEY: misc feature	
LOCATION: (131)..(131)	
OTHER INFORMATION: Xaa	is any amino acid
NAME/KEY: misc feature	
LOCATION: (132)..(132)	
OTHER INFORMATION: Xaa	is any amino acid
NAME/KEY: misc feature	
LOCATION: (133)..(133)	
OTHER INFORMATION: Xaa	is any amino acid
NAME/KEY: misc feature	
LOCATION: (146)..(146)	
OTHER INFORMATION: Xaa	is any amino acid
NAME/KEY: misc feature	
LOCATION: (148)..(148)	
OTHER INFORMATION: Xaa	is any amino acid
NAME/KEY: misc feature	
LOCATION: (160)..(160)	
OTHER INFORMATION: Xaa	is any amino acid
NAME/KEY: misc feature	
LOCATION: (165)..(165)	
OTHER INFORMATION: Xaa	is any amino acid
NAME/KEY: misc feature	
LOCATION: (172)..(172)	
OTHER INFORMATION: Xaa	is any amino acid
NAME/KEY: misc feature	
LOCATION: (183)..(183)	
OTHER INFORMATION: Xaa	is any amino acid
NAME/KEY: misc feature	
LOCATION: (187)..(187)	
OTHER INFORMATION: Xaa	is any amino acid
NAME/KEY: misc feature	
LOCATION: (188)..(188)	
OTHER INFORMATION: Xaa	is any amino acid
NAME/KEY: misc feature	
LOCATION: (189)..(189)	
OTHER INFORMATION: Xaa	is any amino acid
NAME/KEY: misc feature	
LOCATION: (194)..(194)	
OTHER INFORMATION: Xaa	is any amino acid
NAME/KEY: misc feature	
LOCATION: (286)..(286)	
OTHER INFORMATION: Xaa	is any amino acid
NAME/KEY: misc feature	
LOCATION: (306)..(306)	
OTHER INFORMATION: Xaa	is any amino acid
NAME/KEY: misc feature	
LOCATION: (324)..(324)	
OTHER INFORMATION: Xaa	is any amino acid
NAME/KEY: misc feature	
LOCATION: (369)..(369)	
OTHER INFORMATION: Xaa	is any amino acid
NAME/KEY: misc feature	
LOCATION: (431)..(431)	
OTHER INFORMATION: Xaa	is any amino acid
NAME/KEY: misc feature	
LOCATION: (501)..(501)	
OTHER INFORMATION: Xaa	is any amino acid

```

? NAME/KEY: misc feature
? LOCATION: (531)..(531)
? OTHER INFORMATION: Xaa
? is any amino acid
?
? NAME/KEY: misc feature
? LOCATION: (541)..(541)
? OTHER INFORMATION: Xaa
? is any amino acid
?
? NAME/KEY: misc feature
? LOCATION: (584)..(584)
? OTHER INFORMATION: Xaa
? is any amino acid
?
? NAME/KEY: misc feature
? LOCATION: (591)..(591)
? OTHER INFORMATION: Xaa
? is any amino acid
?
? NAME/KEY: misc feature
? LOCATION: (592)..(592)
? OTHER INFORMATION: Xaa
? is any amino acid
?
? NAME/KEY: misc feature
? LOCATION: (594)..(594)
? OTHER INFORMATION: Xaa
? is any amino acid
?
? NAME/KEY: misc feature
? LOCATION: (595)..(595)
? OTHER INFORMATION: Xaa
? is any amino acid
?
? NAME/KEY: misc feature
? LOCATION: (596)..(596)
? OTHER INFORMATION: Xaa
? is any amino acid
?
? NAME/KEY: misc feature
? LOCATION: (611)..(611)
? OTHER INFORMATION: Xaa
? is any amino acid
?
? NAME/KEY: misc feature
? LOCATION: (632)..(632)
? OTHER INFORMATION: Xaa
? is any amino acid
?
? US-09-920-954-1
?

```

Query Match 95.9%; Score 2155; DB 2; Length 639;

Best Local Similarity 96.3%; Pred. No. 4.1e-168;

Sequence	Matches	Mismatches	Indels	Gaps
Conservative	418	0	16	0

Qy	1	NDVARGIVKADVAQSSVGLYGQGGI	VAVADTGLD	TGRNDS	SMHEA	FRGKIT	TALYALGRTN	60			
Db	206	NDVARGIVKADVAQSSVGLYGQGGI	VAVADTGLD	TGRNDS	SMHEA	FRGKIT	TALYALGRTN	265			
Qy	61	NANDTNGHGT	HVAGSVLGNST	TNKGMA	POANLV	QSIIMDS	GGGLGGLPSNLQTLFSQAYS	120			
Db	266	NANDTNGHGT	HVAGSVLGNST	TNKGMA	POANLV	QSIIMDS	GGGLGGLPSNLQTLFSQAYS	325			
Qy	121	AGARIHTNS	WGAAVNGAYTTD	SRNVDDY	VKRN	DWMTIL	FAAGNEGPNGGTISAPGTAKNAI	180			
Db	326	AGARIHTNS	WGAAVNGAYTTD	SRNVDDY	VKRN	DWMTIL	FAAGNEGPNGGTISAPGTAKNAI	385			
Qy	181	TVGATENLR	PSFGSYADN	INHVAQ	FSSRGPT	KDGR	IKPDVMA	PCTFTLSARSSSLAPDSSF	240		
Db	386	TVGATENLR	PSFGSYADN	INHVAQ	FSSRGPT	KDGR	IKPDVMA	PCTFTLSARSSSLAPDSSF	445		
Qy	241	WANHDSKYA	YMGGTSMAT	PIVAGNV	AQLREH	FVKNRGIT	TPKPSLLKAAL	IAGAADIGLGY	300		
Db	446	WANHDSKYA	YMGGTSMAT	PIVAGNV	AQLREH	FVKNRGIT	TPKPSLLKAAL	IAGAADIGLGY	505		
Qy	301	PNGNOG	HGRVTL	DKSLN	VAYWN	ESSLS	TSQKATYSFT	TATAGCP	KLKSLVMSDAPASTTA	360	
Db	506	PNGNOG	HGRVTL	DKSLN	VAYWN	ESSLS	TSQKATYSFT	TATAGCP	KLKSLVMSDAPASTTA	565	
Qy	361	SVTLVND	LDLVI	TAPNGT	QVGVND	FTSPY	NDNWDGR	NNVEN	VFINA	POSQTTYTIEVQAYN	420
Db	566	SVTLVND	LDLVI	TAPNGT	QVGVND	FTSPY	NDNWDGR	NNVEN	VFINA	POSQTTYTIEVQAYN	625
Qy	421	VPVGP	PTQFSL	AIYN	434						
Db	626	VPVGP	QXFS	LAIVN	639						

RESULT 11

RESUB II
US-09-509-814A-2

US-03-003-014A-2
: Sequence 2. Application US/09509814A

; Patent No: 6376227

```

; GENERAL INFORMATION:
; APPLICANT: TAKAIWA, MIKIO
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHISA
; APPLICANT: KUBOTA, HIROMI
; APPLICANT: HITOMI, JUN
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SHIKATA, SHITSUMI
; APPLICANT: NOMURA, MASAFUMI
; TITLE OF INVENTION: ALCALINE PROTEASE
; FILE REFERENCE: 0327-0832-OPCT
; CURRENT APPLICATION NUMBER: US/09/509,814A
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/JP98/04528
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: JP 9-274570
; PRIOR FILING DATE: 1997-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 640
; TYPE: PRP
; ORGANISM: Bacillus sp.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (24)..(24)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (30)..(30)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (33)..(33)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (47)..(47)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (48)..(48)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (54)..(54)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (71)..(71)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (75)..(75)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (90)..(90)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (103)..(103)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (106)..(106)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (129)..(129)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (131)..(131)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (132)..(132)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (133)..(133)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (134)..(134)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (147)..(147)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (149)..(149)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (161)..(161)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (166)..(166)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (173)..(173)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (184)..(184)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (188)..(188)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (189)..(189)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (190)..(190)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (195)..(195)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (287)..(287)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (307)..(307)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (325)..(325)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (370)..(370)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (432)..(432)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (502)..(502)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (532)..(532)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (542)..(542)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (585)..(585)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (592)..(592)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (593)..(593)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (595)..(595)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (596)..(596)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (597)..(597)
; OTHER INFORMATION: Xaa is any amino acid

```

; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (612)..(612)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (633)..(633)
; OTHER INFORMATION: Xaa is any amino acid
US-09-509-814A-2

Query Match 95.9%; Score 2155; DB 2; Length 640;

Best Local Similarity 96.3%; Pred. No. 4,1e-168;

Matches 418; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTCGRNDSMHEAPRGKITALYALGRTN 60

Db 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDTCGRNDSMHEAPRGKITALYALGRTN 266

Qy 61 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120

Db 267 NANDTNGHGHVAGSVLGNSTNKGMAPOANLVFQSIIMDSXGGLGGLPSNLQTLFSQAYS 326

Qy 121 AGARIHTNSGAAVNGAYTTDSNRVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180

Db 327 AGARIHTNSGAAVNGAYTTDSNRVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386

Qy 181 TVGATENLRPSGSIADNINHVAQFSRSGPTKDGRIKPDVMAFGTPIIARSLSLAPDSF 240

Db 387 TVGATENLRPSGSIADNINHVAQFSRSGPTKDGRIKPDVMAFGTPIIARSLSLAPDSF 446

Qy 241 WANHDSKYAYMGTSWATPIVAGNVLAQLREHFVNRGITPKPSLLKAAIAGAADIIGLY 300

Db 447 WANHDSKYAYMGTSWATPIVAGNVLAQLREHFVNRGITPKPSLLKAAIAGAADIIGLY 506

Qy 301 PNGNQGWGRTVLDKSLNVAIVNESSLSSTSQKATYSFTATAGKPLKISLVWSDAPASTTA 360

Db 507 PNGNQGWGRTVLDKSLNVAIVNESSLSSTSQKATYFTATAGKPLKISLVWSDAPASTTA 566

Qy 361 SVTLVNDLVLVTPNGTOYVGNDFTPSYNDWMDGNNVFNAPQSGTITIEVQAYN 420

Db 567 SVTLVNDLVLVTPNGTXVYGNDFKPPXXNXMDGNNVFNINXQSGTITIEVQAYN 626

Qy 421 VPVGPOTFSLAIVN 434

Db 627 VPVGPOTFSLAIVN 640

RESULT 12

US-09-920-954-2

; Sequence 2, Application US/09920954

; Patent No. 6759228

; GENERAL INFORMATION:

; APPLICANT: TAKAIWA, MIKIO

; APPLICANT: OKUDA, MITSUYOSHI

; APPLICANT: SAEKI, KATSUHIKA

; APPLICANT: KUBOTA, HIROMI

; APPLICANT: HITOMI, JUN

; APPLICANT: KAGEYAMA, YASUSHI

; APPLICANT: SHIKATA, SHITSUW

; APPLICANT: NOMURA, MASAFUMI

; TITLE OF INVENTION: ALKALINE PROTEASE

; FILE REFERENCE: 0327-0832-OPCT

; CURRENT APPLICATION NUMBER: US/09/920,954

; CURRENT FILING DATE: 2001-08-03

; PRIOR APPLICATION NUMBER: 09/509,814

; PRIOR FILING DATE: 2000-04-06

; PRIOR APPLICATION NUMBER: PCT/JP98/04528

; PRIOR FILING DATE: 1998-10-07

; PRIOR APPLICATION NUMBER: JP 9-274570

; PRIOR FILING DATE: 1997-06-08

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 640

; TYPE: PRT
; ORGANISM: Bacillus sp.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (24)..(24)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (30)..(30)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (33)..(33)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (47)..(47)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (48)..(48)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (54)..(54)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (71)..(71)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (75)..(75)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (90)..(90)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (103)..(103)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (106)..(106)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (129)..(129)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (131)..(131)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (132)..(132)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (133)..(133)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (134)..(134)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (147)..(147)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (149)..(149)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (161)..(161)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (166)..(166)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (173)..(173)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (184)..(184)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature

121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
327 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
327 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 386
181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTIFLSARSSLAPDSSF 240
181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTIFLSARSSLAPDSSF 240
387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTIFLSARSSLAPDSSF 446
387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTIFLSARSSLAPDSSF 446
241 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGAADIGLGY 300
241 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGAADIGLGY 300
447 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGAADIGLGY 506
447 WANHDSKYAYMGCTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALITAGAADIGLGY 506
301 PNGNQGWGRVTLDKSLNVAIVNNESSLSSTQKATYFTATAGKPLKISLWSDAPASTTA 360
301 PNGNQGWGRVTLDKSLNVAIVNNESSLSSTQKATYFTATAGKPLKISLWSDAPASTTA 360
507 PNGNQGWGRVTLDKSLNVAIVNNESSLSSTQKATYFTATAGKPLKISLWSDAPASTTA 566
507 PNGNQGWGRVTLDKSLNVAIVNNESSLSSTQKATYFTATAGKPLKISLWSDAPASTTA 566
361 SVTLVNDLDELITAPNGTQVGNDFTSPPYNDNDGRNNVENVFINAPQSGTYTIEVOAYN 420
361 SVTLVNDLDELITAPNGTQVGNDFTSPPYNDNDGRNNVENVFINAPQSGTYTIEVOAYN 420
567 SVTLVNDLDELITAPNGTQVGNDFTSPPYNDNDGRNNVENVFINAPQSGTYTIEVOAYN 626
567 SVTLVNDLDELITAPNGTQVGNDFTSPPYNDNDGRNNVENVFINAPQSGTYTIEVOAYN 626
421 VPVGPQTFSLAIVN 434
421 VPVGPQTFSLAIVN 434
627 VPVGPQTFSLAIVN 640
627 VPVGPQTFSLAIVN 640

RESULT 13
US-09-985-689A-6
; Sequence 6, Application US/09985689A
; Patent No. 6803222
; GENERAL INFORMATION:
; APPLICANT: HATADA, YUJI
; APPLICANT: OGAWA, AKINORI
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483USO
; CURRENT APPLICATION NUMBER: US/09/985,689A
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-985-689A-6

Query Match 95.4%; Score 2143; DB 2; Length 434;
Best Local Similarity 93.5%; Pred. No. 2.3e-167;
Matches 406; Conservative 19; Mismatches 9; Indels 0; Gaps 0;
Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 60
Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120
Db 61 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120
Qy 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Db 121 AGARIHTNSWGAAVNGAYTTDSRNVDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
Qy 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTIFLSARSSLAPDSSF 240
Db 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAFGTIFLSARSSLAPDSSF 240

LOCATION: (188)..(188)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
LOCATION: (189)..(189)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
LOCATION: (190)..(190)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
LOCATION: (195)..(195)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
LOCATION: (287)..(287)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
LOCATION: (307)..(307)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
LOCATION: (325)..(325)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
LOCATION: (370)..(370)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
LOCATION: (432)..(432)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
LOCATION: (502)..(502)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
LOCATION: (532)..(532)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
LOCATION: (542)..(542)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
LOCATION: (585)..(585)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
LOCATION: (592)..(592)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
LOCATION: (593)..(593)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
LOCATION: (595)..(595)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
LOCATION: (596)..(596)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
LOCATION: (597)..(597)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
LOCATION: (612)..(612)
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
LOCATION: (633)..(633)
; OTHER INFORMATION: Xaa is any amino acid
US-09-920-954-2

Query Match 95.9%; Score 2155; DB 2; Length 640;
Best Local Similarity 96.3%; Pred. No. 4.1e-168;
Matches 418; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 60
Db 207 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 266
Qy 61 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 120
Db 267 NANDTNGHGHVAGSVLNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFQAYS 326

Qy 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVNKRGITPKPSLLKALIAAGADIGLY 300
Db 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVNKRGITPKPSLLKALIAAGADIGLY 300
Qy 301 PNGQNGRVRTLDKSLNVAQVNETSSSTSKATYSFTATAGKPLKISLVMSDAPASTTA 360
Db 301 PNGQNGRVRTLDKSLNVAQVNETSSSTSKATYSFTATAGKPLKISLVMSDAPASTTA 360
Qy 361 SVTLVNDLDELVTAPNGTQYVGNDFTPYNDNWDGRNNVENVFNAPOSQGYTIEVOAYN 420
Db 361 SVTLVNDLDELVTAPNGTQYVGNDFTPYNDNWDGRNNVENVFNAPOSQGYTIEVOAYN 420
Qy 421 VPVGPQTFSLAIVN 434
Db 421 VPVGPQTFSLAIVN 434

RESULT 14
US-09-985-689A-7
; Sequence 7, Application US/09985689A
; Patent No. 6803222
; GENERAL INFORMATION:
; APPLICANT: HATADA, YUJI
; APPLICANT: OGAWA, AKINORI
; APPLICANT: KAGEYAMA, YASUSHI
; APPLICANT: SATO, TSUYOSHI
; APPLICANT: ARAKI, HIROYUKI
; APPLICANT: SUMITOMO, NOBUYUKI
; APPLICANT: OKUDA, MITSUYOSHI
; APPLICANT: SAEKI, KATSUHIISA
; TITLE OF INVENTION: Alkaline proteases
; FILE REFERENCE: 215483USO
; CURRENT APPLICATION NUMBER: US/09/985,689A
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: JP P2000-355166
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: JP P2001-114048
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-985-689A-7

Query Match 94.6%; Score 2125.5; DB 2; Length 433;
Best Local Similarity 93.5%; Pred. No. 6.2e-166;
Matches 406; Conservative 19; Mismatches 8; Indels 1; Gaps 1;

Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 60
Db 1 NDVARGIVKADVAQNNFGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 60
Qy 61 NANDTNGHGHVAGSVLGNSTKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFQOAYS 120
Db 61 NANDPNGHGHVAGSVLGN-ATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFQOAYS 119
Qy 121 AGARIHTNSGVAAGVAYTTDSRNVDYVRKNDMTILFAAGNEGPGGTTISAPGTAKNAI 180
Db 120 AGARIHTNSGVAAGVAYTTDSRNVDYVRKNDMTILFAAGNEGPGGTTISAPGTAKNAI 179
Qy 181 TVGATENLRPSFGSYADNINHVAQFSRRGPTKDGRIKPDVMAFGTPILSARSSLAPDSSF 240
Db 180 TVGATENLRPSFGSYADNINHVAQFSRRGPTDRGRKPDVMAFGTPILSARSSLAPDSSF 239
Qy 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVNKRGITPKPSLLKALIAAGADIGLY 300
Db 240 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVNKRGITPKPSLLKALIAAGADIGLY 299
Qy 301 PNGQNGRVRTLDKSLNVAQVNETSSSTSKATYSFTATAGKPLKISLVMSDAPASTTA 360

Db 300 PNGQNGRVRTLDKSLNVAQVNETSPLTSOKATYSFTAQAGKPLKISLVMSDAPGSTTA 359
Qy 361 SVTLVNDLDELVTAPNGTQYVGNDFTPYNDNWDGRNNVENVFNAPOSQGYTIEVOAYN 420
Db 360 SLTLVNDLDELVTAPNGTKYVGNDFTPYNDNWDGRNNVENVFNAPOSQGYTIEVOAYN 419
Qy 421 VPVGPQTFSLAIVN 434
Db 420 VPVGPQTFSLAIVH 433

RESULT 15
US-08-873-479-42
; Sequence 42, Application US/08873479
; Patent No. 5891701
; GENERAL INFORMATION:
; APPLICANT: Sloma, Alan
; APPLICANT: Lynne, Christianson
; TITLE OF INVENTION: Nucleic Acids Encoding A Polypeptide
; TITLE OF INVENTION: Having Protease Activity
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5891701c No. 5891701disk of No. 5891701th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,479
; FILING DATE: 12-JUN-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Agris, Cheryl H
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 5251.000-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 641 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-873-479-42

Query Match 94.6%; Score 2125.5; DB 1; Length 641;
Best Local Similarity 93.5%; Pred. No. 1.1e-165;
Matches 406; Conservative 19; Mismatches 8; Indels 1; Gaps 1;

Qy 1 NDVARGIVKADVAQSSYGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 60
Db 209 NDVARGIVKADVAQNNFGLYGQGIIVAVADTGLDGTGRNDSMHEAFRGKITALYALGRTN 268
Qy 61 NANDTNGHGHVAGSVLGNSTKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFQOAYS 120
Db 269 NANDPNGHGHVAGSVLGN-ATNKGMAPQANLVFQSIMDSGGGLGGLPANLQTLFQOAYS 327
Qy 121 AGARIHTNSGVAAGVAYTTDSRNVDYVRKNDMTILFAAGNEGPGGTTISAPGTAKNAI 180
Db 328 AGARIHTNSGVAAGVAYTTDSRNVDYVRKNDMTILFAAGNEGPGGTTISAPGTAKNAI 387
Qy 181 TVGATENLRPSFGSYADNINHVAQFSRRGPTKDGRIKPDVMAFGTPILSARSSLAPDSSF 240

us-10-820-714a-1.ra1

Mon Apr 10 06:49:18 2006

Db	368	TVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYYILSARSSLAPDSSF	447
Qy	241	WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY	300
Db	448	WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADVGLGF	507
Qy	301	PNGNOGWRVTLDKSLNVAYVNESSLSTSQKATYSFTATAGKPLKISLVMSDAPASTTA	360
Db	508	PNGNOGWRVTLDKSLNVAFVNETSPLSTSQKATYSFTAQAGKPLKISLVMSDAPGSTTA	567
Qy	361	SVTLVNDLVLVITAPNGTOYVGNDFTSPYNDNWDGNNVNFVFINAPOSQTYTIEVQAYN	420
Db	568	SLTLVNDLVLVITAPNGTKYVGNDFTPYDNNWDGNNVNFVFINAPOSQTYTIEVQAYN	627
Qy	421	VPVGPOTFSLAIVN	434
Db	628	VPVSPOTFSLAIVH	641

Search completed: April 7, 2006, 09:41:08
Job time : 30 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 7, 2006, 09:38:10 ; Search time 114 Seconds
(without alignment)
2685.959 Million cell updates/sec

Title: US-10-820-714A-1

Perfect score: 2247

Sequence: 1 NDVARGIVKADVAQSSYGLY.....EVQAYNVPGPOTFSLAIVN 434

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	2247	100.0	640	2	Q93UV9_9BACI	Q93UV9 bacillus sp
2	2242	99.8	640	2	Q76L84_9BACI	Q76L84 bacillus sp
3	2183	97.2	639	2	Q9AQR3_9BACI	Q9AQR3 bacillus sp
4	2143	95.4	434	2	Q9AQR0_9BACI	Q9AQR0 bacillus sp
5	1998.5	88.9	433	2	Q9AQR1_9BACI	Q9AQR1 bacillus sp
6	1994.5	88.8	433	2	Q9AQR4_9BACI	Q9AQR4 bacillus sp
7	1987.5	88.5	433	2	Q9AQR2_9BACI	Q9AQR2 bacillus sp
8	870.5	38.7	697	2	Q4NB18_9MICC	Q4NB18 arthrobacte
9	754.5	33.6	711	2	Q6MKR4_BDEBA	Q6MKR4 bdellovibri
10	739.5	32.9	1748	2	Q4NVB5_9DELIT	Q4NVB5 anaeromyxob
11	592	26.3	1088	2	Q4HUY5_GIBZE	Q4HUY5 gibberella
12	580	25.8	2030	2	Q747P6_GEOSL	Q747P6 geobacter s
13	531.5	23.7	1741	2	Q54N84_DICDI	Q54N84 dictyosteli
14	523.5	23.3	1743	1	TAGC_DICDI	Q23868 dictyosteli
15	511.5	22.8	1825	2	Q8T9W1_DICDI	Q8T9W1 dictyosteli
16	497	22.1	1905	1	TAGB_DICDI	P54683 dictyosteli
17	497	22.1	1906	2	Q54M83_DICDI	Q54M83 dictyosteli
18	447	19.9	1752	2	Q9GTN7_DICDI	Q9GTN7 dictyosteli
19	425.5	18.9	1388	2	Q580L9_9TRYF	Q580L9 trypanosoma
20	414	18.4	654	2	Q8U0C9_PYRFU	Q8U0C9 pyrococcus
21	414	18.4	663	2	Q5J1Z5_PYRKO	Q5J1Z5 pyrococcus
22	406.5	18.1	561	2	Q8RBJ2_THETN	Q8RBJ2 thermoanaer
23	398	17.7	1239	2	Q9FBZ4_STRCO	Q9FBZ4 streptomyce
24	381	17.0	430	2	Q8ENV1_OCEIH	Q8ENV1 oceanobacil
25	376	16.7	1253	2	Q9FC06_STRCO	Q9FC06 streptomyce
26	366	16.3	1102	2	P95684_STRAO	P95684 streptomyce
27	363.5	16.2	1208	2	Q82B14_STRAW	Q82B14 streptomyce
28	349	15.5	1245	2	Q9RL54_STRCO	Q9RL54 streptomyce
29	347.5	15.5	444	2	Q9KBJ7_BACHD	Q9KBJ7 bacillus ha
30	346.5	15.4	1139	2	Q82139_STRAW	Q82139 streptomyce
31	346	15.4	1105	2	Q8KKH6_STRVD	Q8KKH6 streptomyce

32 340 15.1 442 2 Q5L3I5 GEOKA Q5L3I5 geobacillus
33 338 15.0 412 2 Q9AER6_THEYO Q9AER6 thermoanaer
34 338 15.0 1237 2 Q8G3T4_STRAZ Q8G3T4 streptomyce
35 337 15.0 412 2 Q8RC68_THETN Q8RC68 thermoanaer
36 337 15.0 1294 2 Q5OHM7_STRSH Q5OHM7 streptomyce
37 336 15.0 795 2 Q5NW24_9ARCH Q5NW24 uncultured
38 332.5 14.8 442 2 Q65IP4_BACLD Q65IP4 bacillus l1
39 328.5 14.6 1220 2 Q9LOA0_STRCO Q9LOA0 streptomyce
40 327.5 14.6 435 2 Q8EMJ3_OCEIH Q8EMJ3 oceanobacil
41 324.5 14.4 818 2 Q79CG2_BACSP Q79CG2 bacillus sp
42 324.5 14.4 824 2 Q45464_BACSP Q45464 bacillus sp
43 320.5 14.3 442 2 Q31788_BACSU Q31788 bacillus su
44 320.5 14.3 891 2 Q93635_THESU Q93635 thermococcu
45 310.5 13.8 806 1 SUBV_BACSU P29141 bacillus su

ALIGNMENTS

RESULT 1
ID Q93UV9_9BACI PRELIMINARY; PRT; 640 AA.
AC Q93UV9;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Protease.
GN Name=PROF;
OS Bacillus sp. KSM-KP43.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=109322;
RN [1]_TaxID=109322;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KP43;
RA Itoh S., Saeki K.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB051423; BAB55674.2; -; Genomic_DNA.
DR PDB; 1WMD; X-ray; A=207-640.
DR PDB; 1WNE; X-ray; A=207-640.
DR PDB; 1WMF; X-ray; A=207-640.
DR MEROPS; S08.123; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept-Bact-C.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF04151; PPC; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 640 AA; 67991 MW; 4BBAF77E9D592C15 CRC64;

Query Match 100.0%; Score 2247; DB 2; Length 640;
Best Local Similarity 100.0%; Pred. No. 4.2e-139;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NDVARGIVKADVAQSSYGLYGQGVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN 60
|||||
DB 207 NDVARGIVKADVAQSSYGLYGQGVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN 266
|||||
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSGGLGGLPSNLQTLFQAYS 120
|||||
DB 267 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSGGLGGLPSNLQTLFQAYS 326
|||||
QY 121 AGARHTNSGAAVNGAYTTDSRNDYDYVRKNDMTILFAAGNPGNGGTISAPGTAKNAI 180
|||||
DB 327 AGARHTNSGAAVNGAYTTDSRNDYDYVRKNDMTILFAAGNPGNGGTISAPGTAKNAI 386
|||||
QY 181 TVGATENLRPSFGSVADNINHNVAQSSRGPTKDGRIKPDVMAPTFILSARSLAPDSGF 240
|||||
DB 387 TVGATENLRPSFGSVADNINHNVAQSSRGPTKDGRIKPDVMAPTFILSARSLAPDSGF 446
|||||

```
QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
DB 447 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 506

QY 301 PNGNQGWGRVTLDKSLNVAIYVNESSLSSTQKATYSFTATAGKPKIKISLVMSDAPASTTA 360
DB 507 PNGNQGWGRVTLDKSLNVAIYVNESSLSSTQKATYSFTATAGKPKIKISLVMSDAPASTTA 566

QY 361 SVTLVNDLDLVTAPNGTQYVGNDFSPYNDWMDGRNNVENVFINAPOSQTYTIEVOAYN 420
DB 567 SVTLVNDLDLVTAPNGTQYVGNDFSPYNDWMDGRNNVENVFINAPOSQTYTIEVOAYN 566

QY 361 SVTLVNDLDLVTAPNGTQYVGNDFSPYNDWMDGRNNVENVFINAPOSQTYTIEVOAYN 420
DB 567 SVTLVNDLDLVTAPNGTQYVGNDFSPYNDWMDGRNNVENVFINAPOSQTYTIEVOAYN 420

QY 421 VPVGPQTFSLAIVN 434
DB 627 VPVGPQTFSLAIVN 640

RESULT 2
Q76L84_9BACI
ID Q76L84_9BACI PRELIMINARY; PRT; 640 AA.
AC Q76L84_
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Protease.
OS Bacillus sp. KSM-9865.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=192495;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KSM-9865;
RA Okuda M., Saeki K., Kobayashi T.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB084155; BAC82522.1; -; Genomic_DNA.
DR HSSP; P00782; LAQN.
DR SMR; Q76L84; 207-640.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_Bact_C.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISIN
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 640 AA; 67940 MW; 421F7A150FF2868F CRC64;

Query Match 99.8%; Score 2242; DB 2; Length 640;
Best Local Similarity 99.8%; Pred. No. 9e-139;
Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDVARGIKVADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB 207 NDVARGIKVADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 266

QY 61 NANDTNGHGTAVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 267 NANDTNGHGTAVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 326

QY 121 AGARHTNSWGAANVGAYTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
DB 327 AGARHTNSWGAANVGAYTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 386

QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSF 240
DB 387 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSF 446

QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
DB 447 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 506
```

```
QY 301 PNGNQGWGRVTLDKSLNVAIYVNESSLSSTQKATYSFTATAGKPKIKISLVMSDAPASTTA 360
DB 507 PNGNQGWGRVTLDKSLNVAIYVNESSLSSTQKATYSFTATAGKPKIKISLVMSDAPASTTA 566

QY 361 SVTLVNDLDLVTAPNGTQYVGNDFSPYNDWMDGRNNVENVFINAPOSQTYTIEVOAYN 420
DB 567 SVTLVNDLDLVTAPNGTQYVGNDFSPYNDWMDGRNNVENVFINAPOSQTYTIEVOAYN 420

QY 421 VPVGPQTFSLAIVN 434
DB 627 VPVGPQTFSLAIVN 640

RESULT 3
Q9AQR3_9BACI
ID Q9AQR3_9BACI PRELIMINARY; PRT; 639 AA.
AC Q9AQR3_
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Protease.
GN Name=PROA;
OS Bacillus sp. 9860.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=133778;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=9860;
RX MEDLINE=20568675; PubMed=11118284; DOI=10.1006/bbrc.2000.3931;
RA Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
RA Horikoshi K.;
RT "Novel oxidatively stable subtilisin-like serine proteases from
RT alkaliphilic Bacillus sp.: enzymatic properties, sequences, and
RT evolutionary relationships.";
RL Biochem. Biophys. Res. Commun. 279:313-319(2000).
DR EMBL; AB046403; BAB21266.2; -; Genomic_DNA.
DR HSSP; P00782; 1SUP.
DR SMR; Q9AQR3; 206-639.
DR MEROPS; S08.123; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_Bact_C.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF04151; PPC; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 639 AA; 68186 MW; 316AF6FFDBE4FF54 CRC64;

Query Match 97.2%; Score 2183; DB 2; Length 639;
Best Local Similarity 96.3%; Pred. No. 6.7e-135;
Matches 418; Conservative 13; Mismatches 3; Indels 0; Gaps 0;

QY 1 NDVARGIKVADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 60
DB 206 NDVARGIKVADVAQSSYGLYGQGIIVAVADTGLDTRNDSSMHEAFRGKITALYALGRTN 265

QY 61 NANDTNGHGTAVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 120
DB 266 NANDTNGHGTAVAGSVLNGSTNKGMAPOANLVFQSIIMDSGGGLGGLPSNLQTLFSQAYS 325

QY 121 AGARHTNSWGAANVGAYTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 180
DB 326 AGARHTNSWGAANVGAYTDSRNVDYVRKNDMTILFAAGNEGNGGTISAPGTAKNAI 385

QY 181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSF 240
DB 386 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSF 445
```

```
QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
DB 446 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 505
QY 301 PNGNGGWRVTLDKSLNVAYNNESSLSQKATYFTATAGKPLKISLVMSDAPASTTA 360
DB 506 PNGNGGWRVTLDKSLNVAYNNESSLSQKATYFTATAGKPLKISLVMSDAPASTTA 565
QY 361 SVTLVNDLDLVITAPNGTYVGNDFTSFYNDNWDGRNNVNFVFNAPQSGTYYIEVOAYN 420
DB 566 SVTLVNDLDLVITAPNGTYVGNDFTSFYNDNWDGRNNVNFVFNAPQSGTYYIEVOAYN 625
QY 421 VVPGPQTFSLAIVN 434
DB 626 VVPGPQTFSLAIVN 639

RESULT 4
Q9AQR0_9BACI PRELIMINARY; PRT; 434 AA.
AC Q9AQR0_9BACI PRELIMINARY; PRT; 434 AA.
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Protease (Fragment).
GN Name=PROE;
OS Bacillus sp. NV1.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=133781;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NV1;
RX MEDLINE=20566875; PubMed=11118284; DOI=10.1006/bbrc.2000.3931;
RA Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
RA Horikoshi K.;
RT "Novel oxidatively stable subtilisin-like serine proteases from
RT alkaliphilic Bacillus sp.: enzymatic properties, sequences, and
RT evolutionary relationships."
RL Biochem. Biophys. Res. Commun. 279:313-319 (2000).
DR EMBL; AB046406; BAB21269.1; -; Genomic_DNA.
DR HSSP; P00782; 1SUP.
DR SMR; Q9AQR0; 1-434.
DR MEROPS; S08.123; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_Bact_C.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF04151; PPC; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
FT NON_TER 1
FT NON_TER 434
SQ SEQUENCE 434 AA; 45294 MW; 83517EDDB74125D2 CRC64;

Query Match 95.4%; Score 2143; DB 2; Length 434;
Best Local Similarity 93.5%; Pred. No. 1.7e-132;
Matches 406; Conservative 19; Mismatches 9; Indels 0; Gaps 0;

QY 1 NDVARGIKVADVAQSSYGLYGQGVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN 60
DB 1 NDVARGIKVADVAQSSYGLYGQGVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN 60
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGLGGLPSNLTLSQAYS 120
DB 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGLGGLPSNLTLSQAYS 120
QY 121 AGARHTNSWGAANGVAYTTDSRNVDYVRKNDMTILPAAGNEGPNGGTISAPGTAKNAI 180
DB 121 AGARHTNSWGAANGVAYTTDSRNVDYVRKNDMTILPAAGNEGPNGGTISAPGTAKNAI 180
```

41

```
QY 181 TVGATENLRPFGSVADNINHVAFSSRGPTKDGRIKPDVMAPGTFFILSARSLAPDSSF 240
DB 181 TVGATENLRPFGSVADNINHVAFSSRGPTKDGRIKPDVMAPGTFFILSARSLAPDSSF 240
QY 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
DB 241 WANHDSKYAYMGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
QY 301 PNGNGGWRVTLDKSLNVAYNNESSLSQKATYFTATAGKPLKISLVMSDAPASTTA 360
DB 301 PNGNGGWRVTLDKSLNVAYNNESSLSQKATYFTATAGKPLKISLVMSDAPASTTA 360
QY 361 SVTLVNDLDLVITAPNGTYVGNDFTSFYNDNWDGRNNVNFVFNAPQSGTYYIEVOAYN 420
DB 361 SVTLVNDLDLVITAPNGTYVGNDFTSFYNDNWDGRNNVNFVFNAPQSGTYYIEVOAYN 420
QY 421 VVPGPQTFSLAIVN 434
DB 421 VVPGPQTFSLAIVN 434

RESULT 5
Q9AQR1_9BACI PRELIMINARY; PRT; 433 AA.
AC Q9AQR1_9BACI PRELIMINARY; PRT; 433 AA.
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Protease (Fragment).
GN Name=PROD;
OS Bacillus sp. SD521.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=133780;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SD521;
RX MEDLINE=20566875; PubMed=11118284; DOI=10.1006/bbrc.2000.3931;
RA Saeki K., Okuda M., Hatada Y., Kobayashi T., Ito S., Takami H.,
RA Horikoshi K.;
RT "Novel oxidatively stable subtilisin-like serine proteases from
RT alkaliphilic Bacillus sp.: enzymatic properties, sequences, and
RT evolutionary relationships."
RL Biochem. Biophys. Res. Commun. 279:313-319 (2000).
DR EMBL; AB046405; BAB21268.1; -; Genomic_DNA.
DR HSSP; Q45670; 1DBI.
DR SMR; Q9AQR1; 1-433.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007280; Pept_Bact_C.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF04151; PPC; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
FT NON_TER 1
FT NON_TER 433
SQ SEQUENCE 433 AA; 45576 MW; 98A2DF18FE660DDC CRC64;

Query Match 88.9%; Score 1998.5; DB 2; Length 433;
Best Local Similarity 87.8%; Pred. No. 5.2e-123;
Matches 381; Conservative 28; Mismatches 24; Indels 1; Gaps 1;

QY 1 NDVARGIKVADVAQSSYGLYGQGVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN 60
DB 1 NDVARGIKVADVAQSSYGLYGQGVAVADTGLDTRNDSSMHEAFRGKITAYALGRTN 60
QY 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGLGGLPSNLTLSQAYS 120
DB 61 NANDTNGHGHVAGSVLNGSTNKGMAPOANLVFQSIMDSGGLGGLPSNLTLSQAYS 120
```



```
QY 1 NDVARGIKADVAQSSVGLYGGQIIVAVADTGLDGTGRNDSSMHEAFRGKITIYALGRTN 60
Db 1 NDVARGIKADVAQSSVGLYGGQIIVAVADTGLDGTGRNDSSMHEAFRGKITIYALGRTN 60
QY 61 NANDTNGHGHVAGSVLNGSTNGKMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
Db 61 NASDPNGHGHVAGSVLNG-ALNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAWN 119
QY 121 AGARIHTNSGAAVNGAYTTDSRVDDYVRKNDMTILFAAGNPGNGGTISAPGTAKNAI 180
Db 120 AGARIHTNSGAAVNGAYTANSRQVDEYVRNNDMTILFAAGNPGNSGTISAPGTAKNAI 179
QY 181 TVGATENLPSFGSYADNTHVAQFSRGTGRIKPDVMAPTILSARSSLAPDSF 240
Db 180 TVGATENYRPSFGSIADNPHIAQFSRGATRGRIKPDVMAPTILSARSSLAPDSF 239
QY 241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 300
Db 240 WANYNSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLY 299
QY 301 PNGNQGWGRVTLKSLNVAIVNNESSLSQKATYSTATAGKPLKISLWSDAPASTTA 360
Db 300 PNGDQGWGRVTLKSLNVAIVNNEATATATGQKATYSFQAQKPLKISLWTDAPGSTTA 359
QY 361 SVTLVNDLVLITAPNGTQVGNDFSPYNDWGDGRNNVENVEINAPQSGTYTIEVQAYN 420
Db 360 SVTLVNDLVLITAPNGTQVGNDFSPYNDWGDGRNNVENVEINAPQSGTYTIEVQAYN 419
QY 421 VPVGPOTFSLAIYN 434
Db 420 VPSGPORFSLAIYH 433
```

RESULT 8

```
Q4NB18_9M1CC
ID Q4NB18_9M1CC PRELIMINARY; PRT; 697 AA.
AC Q4NB18;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Peptidase S8 and S53, subtilisin, kexin, sedolisin.
GN ORFNames=ArthDRAFT_0589;
OS Arthrobacter sp. FB24.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococciaceae; Micrococcaceae; Arthrobacter.
OX NCBI_TaxID=290399;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FB24;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Arthrobacter sp. FB24."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FB24;
RG US DOE Joint Genome Institute (PGF-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Arthrobacter sp. FB24."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAH01000025; EAL94539.1; -; Genomic_DNA.
DR InterPro; IPR000209; Pept S8_S53.
DR Pfam; PF00082; Peptidase S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILISIN_HIS; 1.
DR PROSITE; PS00138; SUBTILISIN_SER; 1.
KW Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 697 AA; 73821 MW; B8924966C67C0714 CRC64;
```

```
Query Match 38.7%; Score 870.5; DB 2; Length 697;
Best Local Similarity 41.4%; Pred. No. 1.1e-48;
Matches 209; Conservative 73; Mismatches 138; Indels 85; Gaps 14;
QY 1 NDVARGIKADVAQSSVGLYGGQIIVAVADTGLDGTGRNDSSMHEAFRGKITIYALGRTN- 59
Db 196 NVVAREILNADVLQNGTGYRGAGEVAVADTGFDTG-DAANPHPAFTGRVQTYALGRTA 254
QY 60 -NANDTNGHGHVAGSVLNGSTN-----KGMAPQANLVFQSIMDSGGGLGGLPSNLQ 112
Db 255 PDKADDPHGHGHVAGSVLGRNSATMGGAIEGTAPELLILQSLDPPNGGLGIPVNLN 314
QY 113 TLFQSAQYSAGARIHTNSWGA-AVNGAYTTDSRVDDYVRKN-DMTILFAAGNPGNG- 167
Db 315 DLFOKYTDDGARVHTNSWGVGLNLPYDASSREIDFVWNHPDQVLCFAAGNDGVGNSD 374
QY 168 -----GTISAPGTAKNAITVGATENLR-----PSFGSY-----ADNINHVA 203
Db 375 GTVDSNSISGSAAKNCITVGASESLRKEFTSYGTYWPGDPFANPVKRDQKANNPDGMV 434
QY 204 QFSRGTGDKRIKPDVMAPTGFIILSARSSLAP-DSSFANHDSKYAYMGGTSMATPIVA 262
Db 435 AFSSRGTGDKRIKPDVMAPTGFIILSARSSLAP-DSSFANHDSKYAYMGGTSMATPIVA 494
QY 263 GNVQALREHFVKNRGITPKPSLLKAALIAGAADIGLY-----PNGNQGWGRVTLDK 314
Db 495 GCAAVLRETILVKNGLNSPSAALVKALLVNGADVLPQYNPSEAGESPNGNSGWRVNLAR 554
QY 315 SLNV-----AYVNSSSLSTQKATYSF-----TATAGKP 344
Db 555 SVVLPGQGNAGLGGGPLEQGEDEFTDIEVEPKVAAGRRNGPAAEPALTAAGVT 614
QY 345 LKISLWSDAPASTTASVTLVNDLVLITAPNGTQVGNDFSPYNDWGDGRNNVENVFI 404
Db 615 LKISLWSDPPGP-----QLQNDLVLILAADGSRHSGSGTTA---GFDRRNVEQVLW 666
QY 405 NAPSQSGTYTIEVQAYNVVPGPQTFS 429
Db 667 TGMPPQGARIVVRAFRITQFPQPYA 691
RESULT 9
Q6MKR4_BDEBA
ID Q6MKR4_BDEBA PRELIMINARY; PRT; 711 AA.
AC Q6MKR4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Subtilisin-like serine protease precursor.
GN OrderedLocusNames=Bd2321;
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164; DOI=10.1126/science.1093027;
RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
RA Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
RT genomic perspective."
RL Science 303:689-692(2004).
DR EMBL; BX842652; CAE80143.1; -; Genomic_DNA.
DR HSSP; P27693; IAH2.
DR GO; GO:000233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000209; Pept S8_S53.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
```



```
DR PROSITE, PS00138; SUBTILASE SER; 1.
KW Complete proteome; Protease; Signal.
FT SIGNAL 1
SQ SEQUENCE 711 AA; 74914 MW; 4930050843357EES CRC64;

Query Match 33.6%; Score 754.5; DB 2; Length 711;
Best Local Similarity 37.9%; Pred. No. 4.8e-41;
Matches 180; Conservative 77; Mismatches 145; Indels 73; Gaps 13;

QY 18 GLYGGOQIVAVADTGLDTRNDSSMHEAFRGKITALLYALGRITNNA-NTNGHGTHVAGSV 76
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 243 GYAGRGQTVSMADTGLDSG-NTGATHODPAGGVISGYPFGLWSKSWSDPMWGHGTHVAGSV 301
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 77 LQNGSTNKG-----APOANLVQSTMDSGGLGLPSNLQTLFSAQYAGARIHTNSWGA 132
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 302 MGRGTASKGLLKGGAEEANVAEGHWSPMKVLSPKSLGDLFEKAFADGARIHTNSWGG 361
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 133 A-VNGAYTTDSRNVDDYVRKN-DMTILFAAGNEGP-----NGGTISAPGTAKNAITV 182
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 362 ARTFGAYDNFAVQVDEWSYANPDMILILFAAGNSGADKNGKGRIDNSMASPGTAKNVLTV 421
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 103 GATENL-----RPSFGSY-ADNINHAQFSSRGPTKDGRIKPD 219
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 422 GASENVTKSGGIQVPIKRAAKDEWPSEPIYSYISDNGNGLAMPSSRGPTTDGRTKPD 481
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 220 VMAPGTFTLSARSSLAPDSSFWANHDSKYVYMGGTSMATPIVAGNVAOLREHFVKNGRI- 278
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 482 IYAPGTNVLSVFSQEKDASPLMGAINKYDVWGGTSMATPLAAGAAATARQVLVLEKLGWK 541
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 279 TPKPSLLKAALTAGAADIGLGY-----PNGNQGRVTLDKSLNVA----- 319
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 542 NPSAALMKATMLHTAVDMYPGQGEIGARGQEIILTRRENSDEGYGRVDVANILGGAT 601
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 320 -YVNESSLSQKATYSTATAGKPLKISLWSDAPASTTASVTLVNDLDTLVIITAPNGT 378
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 602 QFVDRNQVQAQAEVSYEFTLNAPGSLYANLVMTDAPGSANAQAALVNDLDTLVLTPNGQ 661
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 379 QIVGVNDFTSPYNDNDGRNVNFINAPQSGTYTIEVQAYNPV- -GPQTFSL 430
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 662 TLUSDNDHI-----NNLEWIEKSLPAGTYKLVTKVFKVPQKGQAQAYAL 706
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
Q4NVB5_9DELTA PRELIMINARY; PRT; 1748 AA.
AC Q4NVB5;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DE Peptidase S8 and S53, subtilisin, kexin, sedolisin, Nepovirus coat
DE protein, N-terminal: Nepovirus coat protein, N-terminal precursor.
GN ORFNames=AdenDRAFT 3007;
OS Anaeromyxobacter dehalogenans 2CP-C.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
OX NCBI_TaxID=290397;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Anaeromyxobacter
RL dehalogenans 2CP-C."
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Anaeromyxobacter
RL dehalogenans 2CP-C."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.

CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHD01000011; EAL79523.1.; -; Genomic_DNA.
KW Capsid protein; Signal.
FT SIGNAL 1
SQ SEQUENCE 1748 AA; 177411 MW; B1E6DE33BB81DE76 CRC64;

Query Match 32.9%; Score 739.5; DB 2; Length 1748;
Best Local Similarity 40.1%; Pred. No. 1.5e-39;
Matches 192; Conservative 66; Mismatches 154; Indels 67; Gaps 19;

QY 1 NDVARGIVK----ADVAQSSYGLYQGOQIVAVADTGLD-----TGRNDSSMHEAFR 47
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 248 NDTSRWTITQYGPSDSISDRGLDGRGQIVAGTGLDHDACWFRDPICAAAGPMHR---- 304
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 48 GKITALLYALGRITNNDTN-GHGTHVAGSVLGN-----GSTNKGMAQANLVFOSIMDS 100
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 305 -KVAAYLTVG--GDDYDGNLGHGTHVAGTVAGDQPTITGGAAANGMAPCARVVVTDLFLG 361
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 101 GGLGLPSNLQTLFSAQYAGARIHTNSWGAANVAGYTTDSRNVDDYVRKN-DMTILFA 159
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 362 ENWFSPADLAIEFTTYPALGARLHTNSWSSSN-AYDALARSADRFWHEHPDLVLFA 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 160 AGNEGPNGGTISAPGTAKNAITVGATENLRPFGSYADNINHAQFSSRGPTKDGRIKPD 219
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 421 NGNAGPDVGSVGAAPATAKNVSVGATGN-----GLAED---VASFSSHGPAADGRTKPT 472
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 220 VMAPGTFTLSARSSLAPDSSFWANHDSKYVYMGGTSMATPIVAGNVAOLREHFVKN---R 276
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 473 LTPAGVGIVSADSDGTPAS---NNCSTVAF-SGTSMATPAAAGAAALVRQYFEGGFWDPS 527
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 277 GI-----TPKPSLLKAALTAGAADI---GLG-YPNGNCGWGRVTLDKSLNVA----- 319
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 528 GLGSPADARSFAALVKATLVNSAQNVAGENGNGPISTGGGWRINLSNLRFAADAAY 587
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 320 -YVNESSLSQKATYSTATAGKPLKISLWSDAPASTTASVTLVNDLDTLVIITAPNG 377
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 588 LDVVEVAAAGLETGGSFTRQVFTGAQPLKLVMTDAPGSQLADRSVLNDLDTLVLTPVG 647
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 378 -TQYGVNDFT---SPYNDNDGRNVNFINAPQSGTYTIEVQAYNPVPGQTFSLAI 432
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 648 ATTYLGNVFALGESVAGGAPDLNVEEQVLLAAPTGYTVRTGYNVPGVPGQPFALVI 706
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
Q4HUY5_GIBZE PRELIMINARY; PRT; 1088 AA.
AC Q4HUY5;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=FG11223.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=229533;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepl Y., Collymore A., Cook A., Cooke P., Corum B., Dearrellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Haggopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kellis C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
```

RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhant P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schuppel R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Fusarium graminearum genome sequence."
RL Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACW01000460; EAA75433.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 1088 AA; 119629 MW; E3B38CB94C07F542 CRC64;

Query Match 26.3%; Score 592; DB 2; Length 1088;
Best Local Similarity 35.6%; Pred. No.4e-30;
Matches 181; Conservative 71; Mismatches 170; Indels 86; Gaps 24;

QY 1 NDVARGIVKADVAQSSYGLCYCQGIIVAVADTGLDTRGNDSSM----HEAFRGKITALYAL 56
DB 581 NDLAARETLNANILALSTSYEGNGQKVCVADTGFQGRKWADEMGILVHPAFNGRVEHLEAL 640
QY 57 GRTTNANDTNGHGHVTHAGSVLNGSTN-----KGMAPQANLVFQST-----MDSGGGLGG 106
DB 641 W-LGDSKDTAGHGHVTHAGSVLNGSTN-----KGMAPQANLVFQST-----MDSGGGLGG 106
QY 107 LPSNL-OTLFSQAYSAGARIHTNSWGA---AVNG--AYTTDSRNVDDYV-RKNDMTILFA 159
DB 700 VPMDLGLQLFSNPYKLGRIHNSNGVKWDAKTQGLGYEQAWDIDKFVIDHQDFVVLVA 759
QY 160 AGNECPNGGT-----ISAPCTAKNAITVGATENLRPPSGSVADN-----INHVAQFS 206
DB 760 AGNNAERAKSKSNHIGAAGSAFNCITVGATGTTTRPNNDYGFEDNEVGAKPMTRINDTAKFS 819
QY 207 SRGPTKD-----GRIPKPDVMAPTFTLSARS-SLAPDS-----SFWANHDSKVAYM 251
DB 820 SRGPTKEGRDINGEYAGRIKPDVVAFCVAILLSAASRAMAKDSNRVWYGTGDDDDWTFM 879
QY 252 GGTSMATPIVAGNVAQLREHFVKNRGITPKPSSLKAALIAGAAD-----IGLGYPNNGN 305
DB 880 SGTSMSTPLVAGCVALLREALKEHGKPKSAALIKALLVNGAVNFSQLGLGLGY-DYDQ 938
QY 306 GWRGVTLDKSLNV-----AYNESSLSSTQ-----KATYS-FTATAGK-PL 345
DB 939 GFRGVRDIDSSISMVKLSFVDGGLKLPEDTQFVAPLRQVPEERMTSSLPVPAGRNRL 998
QY 346 KISLVSWDAPASTTASVTLVNDLVLITAPNGTQYGVNDFTSPYNDWNWGRNNVENVFIN 405
DB 999 TVTILVDPKFAQ---SGLMQNDINLIVLS-GGAERHGMKGKP---GYDHTNNVEKLIWE 1051
QY 406 APOSGTYTIEVQAY-NVPV-GPQTFSLA 431
DB 1052 NVPGETPKIVASIWNNIDVKAPTSFAVA 1079

RESULT 12
Q747P6 GEOSL
ID Q747P6 GEOSL PRELIMINARY; PRT; 2030 AA.
AC Q747P6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin type III domain protein.
GN OrderedLocusNames=GSU3219;
OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
OX NCBI TaxID=35554;

[1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PCA / ATCC 51573;
 RX PubMed=14671304; DOI=10.1126/science.1088727;
 RA Mehe B.A., Nelson K.E., Eisen J.A., Paulsen E.J., Dodson R.J.,
 RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
 RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
 RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
 RA Daviden T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
 RA Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R.,
 RA Van Aken S.E., Lovley D.R., Fraser C.M.;
 RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
 environments.";
 RL Science 302:1967-1969(2003).
 DR EMBL; AE017180; AAR36610.1; -; Genomic_DNA.
 DR HSSP; P27693; 1AH2.
 DR TIGR; GSU3219; -.
 DR GO; GO:0004289; F:subtilase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPRO11635; APHP.
 DR InterPro; IPRO03961; FN_III.
 DR InterPro; IPRO00209; Pept_S8_S53.
 DR Pfam; PF07705; CARDB; 8.
 DR Pfam; PF00041; fn3; 1.
 DR Pfam; PF00082; Peptidase_S8; 1.
 DR PRINTS; PR00723; SUBTILISIN.
 DR PROSITE; PS00137; SUBTILASE_HIS; 1.
 KW Complete proteome.
 SQ SEQUENCE 2030 AA; 207213 MW; ED7ADC27DD141E01 CRC64;
 Query Match 25.8%; Score 580; DB 2; Length 2030;
 Best Local Similarity 34.6%; Pred. No. 5.6e-29;
 Matches 158; Conservative 69; Mismatches 168; Indels 62; Gaps 15;
 QY 18 GLYGGQIIVAVADTGLD-----TGRNDSMHEAFRGKITALVALGRTNANDTNHG 68
 DB 225 GITGAGQIVGIADSGVDYDMPFADPANGALPGCHRKIVG-----YDALTGDHNDVADGH 279
 QY 69 GTHVAGSVLGN---GSTNKGMAPQANLVFQSIIMDSGGGLGGLPSNLQTLFSAQYSAGARI 125
 DB 280 GTHIAGTICDGRPGMPGNGIAPGARIHVDLVGTDTLTG-SLELETVLKKAYDSGARI 338
 QY 126 HTNSWGAANGVATYDSRNVDIV-RKNDWTILFANGNGPNGGTISAPGTAQVALTVGA 184
 DB 339 FNGSWGVD-SGNYDALAAALDDPSWRHKDFLAVFANGNGGPABQTATSPAIAKNATSVVA 397
 QY 185 TENLRSPFSYADNHNHVAQFSRGTGKRIKPDYMACTFTLSARSSILAPDSSFANH 244
 DB 398 TGN-----GTDAAT-----VSAESSVGQAPGRANPSVGAQGGVVARS-----DGLIGSGN 445
 QY 245 DSKYAYMGGTSMATPIVAGNVAQLRBHF-----VKNRGIITPKPSLLKAAIAGAA 294
 DB 446 SGTWA-MSGTSVAAAVTSGAALIRQYFDGFPPTGSPVATNKLQPSAALLKAVLNSAE 504
 QY 295 -----DIGLYPNNGNGWGRVTLDKSL-----NVAYNNESSLSSTSQKATYSFTATAG 342
 DB 505 ALLSDDPGDSKPGKGGWRPKLINTLFFNGDSHSLVVDGGTGLETDGVMQRLYFSPGG 564
 QY 343 KPLKISIAVSDAPASTTASVTLVNDLQDLVITAPNGYQYVGNDFTPVND-----NWDGR 396
 DB 565 RRLKTLTAWDPAAPGATGASPLTNDLNLVVPADPGTYILGNLNCSHGDYESTGTGFSDR 624
 QY 397 NNV-ENVFINAPOSGTYTIEVQAYNPVPGPQTFFSLAI 432
 DB 625 VNVEEQVWIKRPVAGTYLVKVICASIPVGGPQPALVM 661
 RESULT 13
 Q54M84_DICD1
 ID Q54M84_DICD1 PRELIMINARY; PRT; 1741 AA.
 AC Q54M84;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

```

13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE ABC transporter B family protein.
GN Name=tagC; ORFNames=DDR0191192;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szafarski K., Xu Q.,
RA Tungal B., Kummerfeld S., Madera M., Konfortov B.-A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.C.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Linday R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Loulsged H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shalunsky G., Schleicher M., Weinstein G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzner M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
RA "The genome of the social amoeba Dictyostelium discoideum."
RL Nature 0:0-0(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data
CC EMBL; AF101000133; EAL64353.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR011527; ABC membrane 1.
DR InterPro; IPR001140; ABC_TM_transp.
DR InterPro; IPR003439; ABC_transp_like.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF00664; ABC membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR Pfam; PF00082; Peptidase S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00929; ABC_TM1F; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
SQ SEQUENCE 1741 AA; 193684 MW; 44DEC61D68E4947D CRC64;

Query Match 23.7%; Score 531.5; DB 2; Length 1741;
Best Local Similarity 28.1%; Pred. No. 7e-26;
Matches 166; Conservative 81; Mismatches 149; Indels 195; Gaps 24;

QY 19 LVQGGQIVAVDTGLDGTGR---NDS-----SMHEAFRGKITALYALGRTNNDNTNGH 68
D 19 LVQGGQIVAVDTGLDGTGR---NDS-----SMHEAFRGKITALYALGRTNNDNTNGH 68
DB 314 LRKGQILSIADTGLDGSCHFFSDSKYPIPLNSVNLNHR-KVVTYITTTSDSDSKVDGH 372
QY 69 GTHVAGSVLG-----NGSTNKGMAPOANLVFQSIMDSGGGLGL-PSNLQTLFSQAY 119
D 69 GTHVAGSVLG-----NGSTNKGMAPOANLVFQSIMDSGGGLGL-PSNLQTLFSQAY 119
DB 373 GTHICGAAGTPESSVNLISFSGSLADAKIAF---FDLASGSSSLTPPSDLKQLYQPLY 429
QY 120 SAGARHTNSWGA-----AVNGAYTDSRVDDYVRKN-DMTILFAAGNEGPNGGTIS--A 172
D 120 SAGARHTNSWGA-----AVNGAYTDSRVDDYVRKN-DMTILFAAGNEGPNGGTIS--A 172
DB 430 DAGARVHCDSWGVSVEGYTGSYSSTASIDDFLFTHPDIIILRAAGN--NEQVLSLIT 486

```

DR pfam; PF00082; Peptidase S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR Prodom; PD00006; ABC transporter; 1.
DR PROSITE; PS00219; ABC TRANSPORTER_1; 1.
DR PROSITE; PS00211; ABC TRANSPORTER_2; 1.
DR PROSITE; PS00893; ABC TRANSPORTER_3; 1.
DR PROSITE; PS00136; SUBTILASE ASP; FALSE_NEG.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; FALSE_NEG.
KW ATP-binding; Glycoprotein; Hydrolase; Nucleotide-binding; Protease;
KW Serine protease; Signal; Transmembrane; Transport.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 1743 Prestalk-specific protein tag.
FT TRANSMEM 962 982 Potential.
FT TRANSMEM 1027 1047 Potential.
FT TRANSMEM 1072 1092 Potential.
FT TRANSMEM 1157 1177 Potential.
FT TRANSMEM 1260 1280 Potential.
FT TRANSMEM 1288 1308 Potential.
FT DOMAIN 1031 1314 ABC transmembrane type-1.
FT DOMAIN 1450 1687 ABC transporter.
FT NP_BIND 1485 1492 ATP (Potential).
FT REGION 316 642 Serine protease.
FT COMBIAS 42 46 Poly-Asn.
FT COMBIAS 94 103 Poly-Asn.
FT COMBIAS 643 646 Poly-Ala.
FT COMBIAS 733 741 Poly-Asn.
FT COMBIAS 786 792 Poly-Ser.
FT COMBIAS 1337 1340 Poly-Glu.
FT COMBIAS 1346 1352 Poly-Gly.
FT COMBIAS 1353 1357 Poly-Asn.
FT COMBIAS 1358 1364 Poly-Asp.
FT COMBIAS 1381 1386 Poly-Asn.
FT COMBIAS 1707 1729 Poly-Asn.
FT ACT_SITE 325 325 Charge relay system (By similarity).
FT ACT_SITE 372 372 Charge relay system (By similarity).
FT ACT_SITE 637 637 Charge relay system (By similarity).
FT CARBOHYD 390 390 N-linked (GlcNAc..). (Potential).
FT CARBOHYD 536 536 N-linked (GlcNAc..). (Potential).
FT CARBOHYD 547 547 N-linked (GlcNAc..). (Potential).
FT CARBOHYD 614 614 N-linked (GlcNAc..). (Potential).
FT CARBOHYD 689 689 N-linked (GlcNAc..). (Potential).
FT CARBOHYD 735 735 N-linked (GlcNAc..). (Potential).
FT CARBOHYD 741 741 N-linked (GlcNAc..). (Potential).
FT CARBOHYD 776 776 N-linked (GlcNAc..). (Potential).
FT CARBOHYD 832 832 N-linked (GlcNAc..). (Potential).
FT CARBOHYD 887 887 N-linked (GlcNAc..). (Potential).
FT CARBOHYD 1251 1251 N-linked (GlcNAc..). (Potential).
FT CARBOHYD 1385 1385 N-linked (GlcNAc..). (Potential).
FT CARBOHYD 1386 1386 N-linked (GlcNAc..). (Potential).
FT CARBOHYD 1454 1454 N-linked (GlcNAc..). (Potential).
FT CARBOHYD 1704 1704 N-linked (GlcNAc..). (Potential).
SQ SEQUENCE 1743 AA; 194146 MW; 12DB363E2F729839 CRC64;
Query Match 23.3%; Score 523.5; DB 1; Length 1743;
Best Local Similarity 27.9%; Pred. No. 2.3e-25;
Matches 165; Conservative 81; Mismatches 150; Indels 195; Gaps 24;
QY 19 LYGGQGVAVADTGLDTRG---NDS-----SMHEAFRGKITALVALGRNTNANDTNGH 68
DB 314 LRKGQGLSIADTGLDGSCHFFSDSKYPIPLNSVLNHR-KVVTYTTSTSDSDKVDGH 372
QY 69 GTHVAGSVLG-----NGSTNKGMAPQANLVFQSIMDSGGGLGGL--PSNLQTLFQAY 119
DB 373 GTHICGSAAGTPEDSSVNISSFSGLATDAKIAF---FDLASGSSSLTPPSDLKQLYQPLY 429
QY 120 SGARIHTNSWGA-----AVNGAYTDSRVNDVYRKN-DMTILPAAGNEGPGNGTIS--A 172
DB 430 DAGARVHCDSWGSVSVEGTGYSSTASIDDFLTHPDFFILRAAGN---NEQYLSLIT 486
QY 173 PGTAKNAITVGATENLR-----PSFGSYADNI----- 199
DB 487 QSTAKNVIITGAHQTHENYLTGPNYINQSSVDINQBELCDFDSRYCNYTTAQCCLES 546

200 -----NHVAFSSRGPTKGRKIPDVWAPGTFIL 228
547 NATTTGLASCCPTLLRKSVIDAANTOPLLYNNENICSFSSKGPHTDGRMKPALVAPGEYIT 606
229 SARSSLA-----PDSSFWANDSKYAYMGSTMATPIVAGNVNAQREH-----F 272
607 SANSNGANTDQCGDGL-PNTNALLA-ISGTSMATSPAAAATLILRQVLVDGYPTGSI 664
273 VNRGITPKPSLLKALIAAG-----ADIGLYPNGN-----QGWGRVT 311
665 VESNKLPQPTGSLKALMINNAQLNGTFLQITSSSITPSNQVFENFAGASLVQGWGAIR 724
312 LDKSLNVAVVNESS-----SLSTSOKATYSPT-- 338
725 MSNWLHVNNNNNNNNNNKTSDDGITRFDGIGGLDLRLVKPNQWKEESLSTGQNTSYCTYK 784
339 -----ATAGKPLK--ISLWSDAPASTTASVTLVNDLDLVI-----TAPNGT 378
785 PSSSSSSNGNIPRVVATLVWTDPSYAGAKFNVLNNLDLTWIIYRDNGSTIFSYNQGS 844
379 QVGVNDFTSPYNDWGRNVNFINAPQSGTYTIEVQAYNVVPGPQTF 429
845 SFLG---LAPTQDT---LNNVEGIVHNPTPEMTYRFVWAGTNPVMPGNF 889

RESULT 15
Q8T9W1_DICDI PRELIMINARY; PRT; 1825 AA.
AC Q8T9W1;
DT 01-JUN-2002 (TREMELrel. 21, Created)
DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
DT 10-MAY-2005 (TREMELrel. 30, Last annotation update)
DE Serine protease/ABC transporter TagD (ABC transporter B family protein).
GN Name=tagD; ORFNames=DOB0191427;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_Taxid=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Anjard C., Loomis W.F.;
RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RL [2]
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sucgang R., Barriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Pey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny J., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchreiser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Lousaged H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodcock J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer B., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
RA "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2003).
DR EMBL; AF466309; AAL74253.1; -; Genomic DNA.
DR EMBL; AAF01000133; EAL64354.1; -; Genomic DNA.
DR HSSP; P08716; 1MT0.
DR DictyBase; DDB0191427; tagD.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.

DR GO: GO:0016887; F:ATPase activity; IEA.
DR GO: GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0004289; F:subtilase activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR003593; AAA ATPase.
DR InterPro: IPR011527; ABC_membrane_1.
DR InterPro: IPR001140; ABC_TM_transp.
DR InterPro: IPR003439; ABC_transp_like.
DR InterPro: IPR002029; Pept_S8_S53.
DR Pfam: PF00664; ABC_membrane; 1.
DR Pfam: PF00005; ABC_tran; 1.
DR Pfam: PF00082; Peptidase_S8; 1.
DR PRINTS: PR00723; SUBTILISIN.
DR ProDom: PD000006; ABC_transporter; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS0929; ABC_TM1F; 1.
DR PROSITE: PS0211; ABC_TRANSPORTER_1; 1.
DR PROSITE: PS0893; ABC_TRANSPORTER_2; 1.
DR PROSITE: PS00137; SUBTILASE_HIS; UNKNOWN_1.
DR PROSITE: PS00138; SUBTILASE_SER; UNKNOWN_1.
KW Protease.
SQ SEQUENCE 1825 AA; 202642 MW; E28160BC78613A3B CRC64;

Query Match 22.8%; Score 511.5; DB 2; Length 1825;
Best Local Similarity 27.9%; Pred.No.1.5e-24;
Matches 164; Conservative 76; Mismatches 155; Indels 193; Gaps 22;

QY 19 LYGOQIVAVADTGLDGTGR---NDS-----SMHEAFEGKITALYALGRNTNNANDTNGH 68
DB 327 LRGKQLLSIADTGLDGHCFSDSDNNPIPNVSNLNRKVVYIGSL--HDNEDYVDGH 384
QY 69 GTHVAGSVLNG-----STNKGMAPQANLVFQSI-MDSGGGLGGLPSNLQTLFSQAYS 120
DB 385 GTHVCGSAAAGPEDSSLAISFSGLATDAKIAFFDLASDPNNPVPPEQYQLYQLYN 444
QY 121 AGARIHTNSGA-----AVNGATTDSRNVDVYRKN-DWTILFAAGNEGNGGTISAPGT 175
DB 445 AGARVHGDSWGSLSIQYLGYSDDAGSIDDFLYTHPDFIILRAAGNEQYSSLLS-QAT 503
QY 176 AKNAITVGATENLRPSF-----192
DB 504 AKNVITVGAETHSYTTDALEYSNFETVAKSTLNSLCQSFDDKVCYTTTAQCCTEYST 563
QY 193 -----GSYAD-----NINHVAQFSRGPTKGRKPDVMAPGTFILSA 230
DB 564 VKGLSGCCTSYIKNSYASIFSSQPELYNENNICSFSSKGPETHDRLKPDIVAPGOVITSA 623
QY 231 RSSLA-----PDSSFANHDSKYAYMGGTSMATPIVAGNVAQLREH-----271
DB 624 RSGNANTTDQCGDGLPNTNALLSE-----SGTSMATPLATAATTILRQYLVGYPT 676
QY 272 --FVKNRGITPKPSLLKALIAAGADIGLGP-----NGNGQWGRV 310
DB 677 GSIVSNKLUPTGCSLLKALMINNAQLNGTFFLSSINTNPSNAVFTTFAGANFVQWGSLL 736
QY 311 TLDKSLNAVYVNESS-----SLTSQKATYSFT-----338
DB 737 RMSEWL---YVESGKPKPSRWVGIGELGDKKASNWKEYSLSTGQNVSYCYFTYKPSSS 793
QY 339 --ATAGKP-LKISLWSDAPASTASVTLYNDLDLVITAPNGTQ----YVGNDFTSYND 391
DB 794 GNSGGIPRIVATLVMTDPPSYSGAKNLVNNLDLTMT---NTESEFIFYNSGGSSYNG 850
QY 392 N-----WGRNNVENVF---INAPQSTYTIETVQAYNVVPQPOTFS 429
DB 851 TKGTTLPLQDSINNVEGIYTPINTKSEISFRFIAGTNIPIGPQNFS 898